

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:12:27 ; Search time 12.0425 Seconds
(without alignments)
1509.673 Million cell updates/sec

Title: US-09-811-367B-1
Perfect score: 1023
Sequence: 1 MTSVSYSMLEPLTATQAN.....GLQASCEVPLHGVCKKVR L 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: Piri:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	525.5	51.4	188	2 I59421	mast cell function
2	201	19.6	225	2 I38700	hNKR-P1a protein -
3	193	18.9	257	2 I50146	gene 17.5 protein
4	191	18.7	227	2 A46467	natural killer cell
5	190	18.6	233	2 P70372	natural killer cell
6	182	17.8	231	2 P70374	natural killer cell
7	180	17.6	216	2 P70375	natural killer cell
8	178.5	17.4	240	2 I54524	natural killer cell
9	176	17.2	404	2 A46274	HIV gp120-binding
10	175.5	17.2	223	2 A35917	NK-cell receptor p
11	174.5	17.1	304	2 JX0209	lymphocyte early a
12	174	17.0	199	2 JH0822	type II lectin-like
13	169	16.5	237	2 JH7608	asialoglycoprotein
14	167	16.3	301	2 S13165	C type lectin, B 1
15	166	16.2	156	2 T28141	asialoglycoprotein
16	165	16.1	284	2 S29855	lectin M-ASGP-BP p
17	164.5	16.1	306	2 A42230	T-cell surface gly
18	162	15.8	262	2 A30573	T-cell surface gly
19	162	15.8	262	2 A45813	NKR-P1 protein hom
20	160.5	15.7	223	2 B46467	hepatic lectin 2 -
21	160.5	15.7	284	1 LNRT2	hepatic lectin 2 -
22	160.5	15.7	301	1 LNRT2	hepatic lectin H1
23	157.5	15.4	291	1 LNRT1	natural killer cell
24	157	15.3	262	2 I49361	phospholipase-A(2)
25	156	15.2	1487	2 S48719	hepatic lectin hom
26	153.5	15.0	167	1 WVVZF2	Ly-49D-GE antigen
27	151.5	14.8	260	2 I49049	natural killer cell
28	149	14.6	170	2 T28140	NKR-P1 protein hom
29	148.5	14.5	220	2 C46467	

30	148.5	14.5	550	2 A28166	Kupffer cell recep
31	146.5	14.3	1326	2 B56395	secretory phosphol
32	146.5	14.3	1465	2 A56395	secretory phosphol
33	146	14.3	311	1 LNRT2A	asialoglycoprotein
34	145.5	14.2	1479	2 T42710	mannose receptor,
35	143.5	14.0	144	2 PC7027	aggratin alpha cha
36	142	13.9	146	2 JC7135	agkissacutacin beta
37	141.5	13.8	1458	1 A49707	phospholipase A2 r
38	140.5	13.7	267	2 I49053	Ly-49G.2 antigen -
39	140.5	13.7	280	2 I49052	chondroitin sulfat
40	139.5	13.6	3562	2 A47171	phospholipase A2 r
41	138.5	13.5	1463	2 A53210	pancreatitis-assoc
42	137.5	13.4	175	2 S29822	pancreatic stone p
43	137	13.4	165	2 A28351	natural killer cel
44	137	13.4	266	2 I49363	scavenger receptor
45	137	13.4	742	2 JC7595	

ALIGNMENTS

RESULT 1

I59421
mast cell function associated antigen - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I59421
R;Guthmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A;Title: A secretion inhibitory signal transduction molecule on mast cells is another C
A;Reference number: I59421; MUID:96016176; PMID:7568140
A;Accession: I59421
A;Status: preliminary; translated from GE/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-188 <RES>
A;Cross-references: EMBL:X79812; NID:g1020141; PIDN:CAA56208.1; PID:g1020142
C;Genetics:
A;Gene: mafa

Query Match 51.4%; Score 525.5; DB 2; Length 188;
Best Local Similarity 53.5%; Pred. No. 4.8e-42;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

Qy	1	MTSVSYSMLEPLTATQANDYGPQOKSSSKSCSCICVAITLGLTAVLLSVLLYQWIL	60
Db	1	MAUNSIYSTLELPAPRVQDSRWKRVAVLHRCVSVLYVWVALGLLTVILMSLLLYQETL	60
Qy	61	COGSNYSTCASCPDRWMKYGNHCYFFSVEEKDWNSSLEFFCLARDSHLIVITDNQEMS	120
Db	61	CCSGKGFMCQCSRCPCNLWENGSHCYFFSWEKEDWNSSLKFCADKGSLLTFFPDQGVN	120
Qy	121	LLQVFLSEATCWIGLRNNSWRWEDGSPFNPSRISNSFVQTCAINKNGLOASCEVPL	180
Db	121	LFQYVGDEFYWIGLRIDGWRWEDGSPALSLS-ILSNSVYQKCGTIHRCGLHASSCEVAL	179
Qy	181	HGVCKV	187
Db	180	QWICEK	186

RESULT 2

I38700
hNKR-P1a protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C;Accession: I38700
J;Lanier, L.L.; Chang, C.; Phillips, J.H.
J. Immunol. 153, 2417-2428, 1994
A;Title: Human NKR-P1A: A disulfide-linked homodimer of the C-type lectin superfamily e
A;Reference number: I38700; MUID:94358407; PMID:8077657
A;Accession: I38700
A;Status: preliminary; translated from GE/EMBL/DBJ
A;Molecule type: mRNA

A:Residues: 1-225 <RES>
A:Cross-references: EMBL:U11276; NID:G538270; PIDN:AAA21605.1; PID:G544496
A:Superfamily: natural killer cell receptor P1; C-type lectin homology
F:94-210/Domain: C-type lectin homology <LCH>

Query Match 19.6%; Score 201; DB 2; Length 225;
Best Local Similarity 26.0%; Pred. No. 1.7e-11;
Matches 58; Conservative 36; Mismatches 81; Indels 48; Gaps 8;

QY 1 MTDSVIYSMLELPTATQAQNDYGPQKSSSKP-----SCSLVAITLG 44
Db 1 MQQAIYAEINLPT-----DSGPSSSPSLRDVCOQSPWHQFALKLSGAIILLVL- 53
QY 45 LITAVLLSVLLYQWILCOGSNTSTCA-----SCPSCPDWMKYGNHCYFYS 90
Db 54 VVTGLSVSYT-----SLIQKSSIEKCSVDIQSQSNKKTTPRGLNCPFIYMQQLREKLLFS 109
QY 91 VEEKDWNSSLEFLCLARDSHLLVITDQMSLLQVFLSE--AFCWIGLR---NNSGWRWED 145
Db 110 HTVNPWNNSLADCSLKESLLIRDKDELIHTQNLIRDKAILFWIGLNFSLSEKNKWN 169
QY 146 GSPLNFS--RISSNFPVPCGAINKNGLOASCEVPLHGVCCK 186
Db 170 GSFLNSDLIRKDAKENSICISQTSVYSEYCESTEIRWICOK 212

RESULT 3
150146
gene 17.5 protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: 150146
R:Bernot, A.; Zoorob, R.; Auffray, C.
A:Title: Linkage of a new member of the lectin supergene family to the chicken Mhc genes
A:Reference number: 150146; MUID:94164691; PMID:8119728
A:Accession: 150146
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-257 <BER>
A:Cross-references: GB:M89072; NID:G505324; PIDN:AAA48558.1; PID:G505325
A:Superfamily: C-type lectin homology
F:129-241/Domain: C-type lectin homology <LCH>

Query Match 18.9%; Score 193; DB 2; Length 257;
Best Local Similarity 26.6%; Pred. No. 1.1e-10;
Matches 49; Conservative 28; Mismatches 89; Indels 18; Gaps 4;

QY 17 QAQNDYGPQKSSSKPSCSL-----VAITGLLTAVLLSVLLYQWILCOGSNYSTC 69
Db 64 EATTREGDEERQSGSGSELRQNRRLVCLVALSAVPCMLVALVAVIVLQRP-----C 119
QY 70 ASCPS---CPDRWMKYGNHCYFYSVEEKDWNSSLEFLCLARDSHLLVITDQMSLLQV 125
Db 120 SPRPFVSHVCNANWVGFOCKYIFSDTSQDWNSSREHCHRLGASLATIDTKEEFMLQY 179
QY 126 LSEAFPCWIGLRNNSG---WRWEDGSPNFSNFSFVQTCGAINKNGLOASCEVPLHG 182
Db 180 QRPADRWIGLHRAEGDEHTWADGSAFTNRPVFLRGGRCAYLNGDGISSALCHSEKFW 239
QY 183 VCKK 186
Db 240 VCSR 243

RESULT 4
A46467
natural killer cell receptor P1 - mouse
N:Alternate names: NKR-P1 protein
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 19-Feb-1999 #text_change 05-May-2000
C:Accession: A46467; A46502; A46456
R:Giorda, R.; Trucco, M.

J. Immunol. 147, 1701-1708, 1991
A:Title: A family of genes selectively coexpressed in adherent lymphokine-activated ki
A:Reference number: A46467; MUID:91349596; PMID:1880421
A:Accession: A46467
A:Molecule type: mRNA
A:Residues: 'MHLLCT', 1-227 <GIO>
A:Cross-references: GB:M77676; NID:G200058
A:Experimental source: A-LAK cells, C57BL
A:Note: sequence extracted from NCBI backbone (NCBIN:52378, NCBIP:52379); the sequence
R:Giorda, R.; Weisberg, E.P.; Ip, T.K.; Trucco, M.
J. Immunol. 149, 1957-1963, 1992
A:Title: Genomic structure and strain-specific expression of the natural killer cell
A:Reference number: A46502; MUID:92388663; PMID:1517565
A:Accession: A46502
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-109, 'H', '111-181', 'D', 183-227 <GI2>
A:Cross-references: GB:X64716; NID:G53395; PIDN:CAA45971.1; PID:G817989
A:Experimental source: BAUB/c 373 fibroblastoid cell line
A:Note: sequence extracted from NCBI backbone (NCBIN:113037, NCBIN:113063, NCBIN:113072)
R:Yokoyama, W.M.; Ryan, J.C.; Hunter, J.J.; Smith, H.R.; Stark, M.; Seaman, W.E.
J. Immunol. 147, 3229-3236, 1991
A:Title: cDNA cloning of mouse NKR-P1 and genetic linkage with LY-49. Identification of
A:Reference number: A46456; MUID:92013158; PMID:1680927
A:Accession: A46456
A:Molecule type: mRNA
A:Residues: 1-38, 'L', 40-227 <YOK>
A:Cross-references: GB:M77753; NID:G198569; PIDN:AAA39366.1; PID:G198570
A:Note: sequence extracted from NCBI backbone (NCBIN:60429, NCBIP:60431)
C:Superfamily: natural killer cell receptor P1; C-type lectin homology
F:94-210/Domain: C-type lectin homology <LCH>

Query Match 18.7%; Score 191; DB 2; Length 227;
Best Local Similarity 27.4%; Pred. No. 1.5e-10;
Matches 49; Conservative 43; Mismatches 71; Indels 16; Gaps 7;

QY 24 PQKSSSKPSCSLVAITGLT-PAVLLSVLLYQ-----WILCOGS-NYST-CASCPS 74
Db 34 PRSHRSALKSLCAGLILVVLIGMSVLRVLIQPSIEKCYVLLIQENLNKTTDCSAKLE 93
QY 75 CPDRWMKYGNHCYFYSVEEKDWNSSLEFLCLARDSHLLVITDQMSLLQVFLSEAF--CW 132
Db 94 CPQDWLSHRDKCFHVSQVSNVTWEEGLVDCDCKGATMLIQDEELRFLDLSIKEKYNFW 153
QY 133 IGLR---NNSGWRWEDGSPNFS--RISSNFPVTCGAINKNGLOASCEVPLHGVCCK 186
Db 154 IGLRYTLPMNWKWINGSTLNSDLKITGDTENDSCAISAISGDKVTFESCNSDNRWICOK 212

RESULT 5
PT0372
natural killer cell receptor group 2, splice form A - human
N:Alternate names: NKG2-A; NKG2-B
N:Contains: natural killer cell receptor group 2, splice form B
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-May-2000
C:Accession: PT0372; PT0373
R:Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
J. Exp. Med. 173, 1017-1020, 1991
A:Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type I
A:Reference number: PT0372; MUID:91178434; PMID:2007850
A:Accession: PT0372
A:Molecule type: mRNA
A:Residues: 1-233 <HOU1>
A:Cross-references: EMBL:X54867; NID:G35056; PIDN:CAA38649.1; PID:G35057
A:Experimental source: natural killer cell
A:Accession: PT0373
A:Molecule type: mRNA
A:Residues: 1-95, 114-233 <HOU2>
A:Cross-references: GB:X54868; NID:G35058; PIDN:CAA38650.1; PID:G35059
A:Experimental source: natural killer cell
C:Genetics:
A:Gene: GDB:KLCR1; NKG2

A;Cross-references: GDB:138773; OMIM:161555
A;Map position: 12pter-12qter
C;Superfamily: natural killer cell receptor P1; C-type lectin homology
C;Keywords: alternative splicing; glycoprotein; transmembrane protein
F;71-98/Domain: transmembrane #status predicted <TRA>
F;119-229/Domain: C-type lectin homology <LCH>
F;102,103,151,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;119-130,147-229,208-221/Disulfide bonds: #status predicted

Query Match 18.6%; Score 190; DB 2; Length 233;
Best Local Similarity 27.8%; Pred. No. 1.1e-10;
Matches 55; Conservative 35; Mismatches 86; Indels 22; Gaps 8;

QY 5 VIYSMLELPATQAQNDYGPQKSSSK--PSC-SCLVAITLGLTAVLL-----SVLLYQ 57
Db ITYAEMLQKASQ---DFQNDKTYHCKDLPSPAPEKLIVGLIGLILMASVVTVIIP 94
QY 58 WILQCGSNYST-----CASCPCPDWRMKYGNHCYFVVEEKDWNSSLEFCLARDSHL 110
Db STLIQRHNSLSNTRTKARHGCHPEWITYNSCYIIGKERTWEESLLACTSKNSSL 154
QY 111 LVITDQEMSLQLVFLSEAFWIGL--RNNSGRWEDGSPNFSR--ISSNSFVOTCGAIN 167
Db LSIDNEEMKFLSIIPSS--WIGVFRNSHHPPWTWNGLAFAKHEIKDSNAELNCAVLQ 212
QY 168 KNGLOASSCEVPLHGVC 185
Db 213 VNRLKSAQCSSIIYHCK 230

RESULT 6
PT0374
natural killer cell receptor group 2-C, splice form 1 - human
N;Alternate names: NKG2-C
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 19-May-2000
C;Accession: PT0374
R;Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
J. Exp. Med. 173, 1017-1020, 1991
A;Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type II
A;Reference number: PT0372; MUID:91178434; PMID:2007850
A;Experimental source: natural killer cell
A;Note: translation of nucleotide sequence is not complete
C;Keywords: transmembrane protein

Query Match 17.8%; Score 182; DB 2; Length 231;
Best Local Similarity 27.8%; Pred. No. 1.1e-09;
Matches 47; Conservative 32; Mismatches 76; Indels 14; Gaps 5;

QY 24 PQKSSSSKPCSCCLVAITLGLTAVLLSVLLYQWILCOGSNYST-----CASCPCPDWR 79
Db PPEKLTAEVLGIICIV-----LMATVLKTVLIPFLFQNNSSPNTTQKARHCHGCPFEW 121
QY 80 MKYGNHCYFVVEEKDWNSSLEFCLARDSHLIVITDQEMSLQLVFLSEAFWIGL--RNN 138
Db ITYNSCYIIGKERTWEESLLACTSKNSSLISIDNEEIKFLASILPSS--WIGVFRNS 179
QY 139 SGWRWEDGSPNFSR--ISSNSFVOTCGAINKNGLOASSCEVPLHGVC 185
Db SHHPVWTWINGLAFAKHKTDSNAELNCAVLQVRLKSAQCSSMIYHCK 228

RESULT 7
PT0375
natural killer cell receptor group 2-D - human
N;Alternate names: integral membrane protein NKG2-D
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-May-2000
C;Accession: PT0375; S15671; S19110
R;Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
J. Exp. Med. 173, 1017-1020, 1991
A;Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type I
A;Reference number: PT0372; MUID:91178434; PMID:2007850
A;Accession: PT0375
A;Molecule type: mRNA
A;Residues: 1-216 <HOU>
A;Cross-references: EMBL:X54870; NID:g35062; PIDN:CAA38652.1; PID:g35063
A;Experimental source: natural killer cell
A;Note: translation of nucleotide sequence is not complete
C;Keywords: transmembrane protein

Query Match 17.6%; Score 180; DB 2; Length 216;
Best Local Similarity 26.8%; Pred. No. 1.1e-09;
Matches 42; Conservative 31; Mismatches 52; Indels 32; Gaps 5;

QY 37 CLVAITLGL-----LLTAVLLSVLLYQWILCOGSNYSTCASCPCPDWRMKYGNHCY 88
Db CFTAVANGIRPITMVAISAVFLNSLENQEVQIP-----LTESYCGCPKRWICYKNICYQ 112
QY 89 FSVEEKDWNSSLEFCLARDSHLIVITDQEMSLQLVFLSEAFWIGL--RNNSGRWED 145
Db FFDESKNWEYSQASCMNQASNLKVKSKEDQDLK--LVKSYHWMGLVHIPTNGSQWED 170
QY 146 GSPINFSRI-----SSNSFVOTCGAIN 167
Db 171 GSTLSPNLLTIEMQKDCALYASSPKGYIENCSTEN 207

RESULT 8
I54524
natural killer cell receptor group 2-C, splice form 2 - human
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 19-May-2000
C;Accession: I54524
R;Adamkiewicz, T.V.; McSherry, C.; Bach, F.H.; Houchins, J.P.
Immunogenetics 39, 218, 1994
A;Title: Natural killer lectin-like receptors have divergent carboxy-termini, distinct
A;Reference number: I54524; MUID:94102823; PMID:8276468
A;Accession: I54524
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-240 <RES>
A;Cross-references: GB:L14542; NID:g292360; PIDN:AAA16833.1; PID:g292361
C;Genetics:
A;Gene: GDB:KLRC2; NKG2-C
A;Cross-references: GDB:9787095
A;Map position: 12p13-12p13
C;Superfamily: natural killer cell receptor P1; C-type lectin homology

Query Match 17.4%; Score 178.5; DB 2; Length 240;
Best Local Similarity 28.6%; Pred. No. 2.4e-09;
Matches 46; Conservative 30; Mismatches 70; Indels 15; Gaps 6;

QY 24 PQKSSSSKPCSCCLVAITLGLTAVLLSVLLYQWILCOGSNYST-----CASCPCPDWR 79
Db PPEKLTAEVLGIICIV-----LMATVLKTVLIPFLFQNNSSPNTTQKARHCHGCPFEW 121
QY 80 MKYGNHCYFVVEEKDWNSSLEFCLARDSHLIVITDQEMSLQLVFLSEAFWIGL--RN 137
Db ITYNSCYIIGKERTWEESLLQACASKNSSLISIDNEEIKFLASILPSS--WIGVFRN 179
QY 138 NSGRWEDGSPNFSR--ISSNSFVOTCGAINKNGLOASSC 176
Db SHHPVWTWINGLAFAKHEIKDSDAERNCAMLHVRGLISDQC 220

RESULT 9

A46274
HIV gp120-binding C-type lectin - human
C:Species: Homo sapiens (man)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-1995
C:Accession: A46274
R:Curtis, B.M.; Scharnowske, S.; Watson, A.J.
Proc. Natl. Acad. Sci. U.S.A. 89, 8356-8360, 1992
A:Title: Sequence and expression of a membrane-associated C-type lectin that exhibits CD
A:Reference number: A46274; MUID:92390446; PMID:1518869
A:Accession: A46274
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-404 <CUR>
A:Experimental source: placenta
A>Note: sequence extracted from NCBI backbone (NCBIN:113134, NCBIPI:113135)
A:Superfamily: C-type lectin homology
F:256-377/Domain: C-type lectin homology <LCH>

Query Match 17.2%; Score 176; DB 2; Length 404;
Best Local Similarity 30.7%; Pred. No. 7e-09; Mismatches 53; Indels 12; Gaps 5;
Matches 39; Conservative 23;
QY 72 CPSCPRMXYGNHCYFVBEKWNSSLEFCLARDSHLLVITDQEMSLQLQVFLSEA-- 129
DB 253 CHPCPWEWTFQGCYFMSQBNWHDITACKVEGAQLVTKSAEQNFLOLQSSRNR 312
QY 130 FCWIGLR--NNSG-WRWEDGSP--NFSRI-----SSNSFVOTCGAINKNGLOQSSCEVP 179
DB 313 FTMGLSLDNOEGTWQWDGSPLLPSFKQYNNRGPNVNBEDCAEFSGNGWDDKCNLA 372
QY 180 LHGVCKK 186
DB 373 KFWICKK 379

RESULT 10

A35917
NK-cell receptor P1 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1999
C:Accession: A35917
R:Giorda, R.; Rudert, W.A.; Vavassori, C.; Chambers, W.H.; Hiserodt, J.C.; Trucco, M.
Science 249, 1298-1300, 1990
A:Title: NKR-P1, a signal transduction molecule on natural killer cells.
A:Reference number: A35917; MUID:90378305; PMID:2399464
A:Accession: A35917
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-223 <GIO>
A:Cross-references: GB:M62891; NID:g205722; PIDN:AAA41710.1; PID:g205723
C:Superfamily: natural killer cell receptor P1; C-type lectin homology
F:94-210/Domain: C-type lectin homology <LCH>

Query Match 17.2%; Score 175.5; DB 2; Length 223;
Best Local Similarity 27.1%; Pred. No. 4.2e-09;
Matches 49; Conservative 44; Mismatches 67; Indels 21; Gaps 9;
QY 24 PQQSSSSKPKSCSLVAITLGLL-TAVLLSVLLYQ-----WILCQGSNYSTCASCPS-- 74
DB 35 PRSHRLALKSLCAGLLILVLAIVGMSILVRVLVQKPSVPCRVLIQ-ENLSKTGS-PAKL 92
QY 75 -CPDRMXYGNHCYFVBEKWNSSLEFCLARDSHLLVITDQEMSLQLQVFLSEA--LSEAF 130
DB 93 KCPKDWLSHRDCKFFVVSQTSITWKSLEADCGGKGATLLVQDQEEIRFLNLTKKISSSF 152
QY 131 CWIGLR--NNSGWRWEDGSP--NFSRI-----SSNSFVOTCGAINKNGLOQSSCEVPVHGVCCK 185
DB 153 -WIGLSYTLSDENWKNWINGSTLNSDVLITGTEDKSCASVSQDKVLSHSCSDNIVWCQ 211
QY 186 K 186

Db 212 K 212

RESULT 11

JX0209
lectin, galactose/N-acetylgalactosamine-specific - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
C:Accession: JX0209; FX0009
R:Sato, M.; Kawakami, K.; Osawa, T.; Toyoshima, S.
J. Biochem. 111, 331-336, 1992
A:Title: Molecular cloning and expression of cDNA encoding a galactose/N-acetylgalactose
A:Reference number: JX0209; MUID:92268032; PMID:1587794
A:Accession: JX0209
A:Molecule type: mRNA
A:Residues: 1-304 <SAP>
A:Cross-references: GB:S36676; NID:g249360; PIDN:AAB22171.1; PID:g249361
R:Oda, S.; Sato, M.; Toyoshima, S.; Osawa, T.
J. Biochem. 104, 600-605, 1988
A:Title: Purification and characterization of a lectin-like molecule specific for galac
A:Reference number: FX0009; MUID:89197865; PMID:3241002
A:Accession: FX0009
A:Molecule type: protein
A:Residues: 102-120/137, 'X', 139-151 <ODA>
C:Superfamily: hepatic lectin; C-type lectin homology
C:Keywords: glycoprotein; lectin; macrophage; transmembrane protein
F:36-61/Domain: transmembrane #status predicted <TRA>
F:173-296/Domain: C-type lectin homology <LCH>
F:74,166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.1%; Score 174.5; DB 2; Length 304;
Best Local Similarity 27.5%; Pred. No. 7.2e-09;
Matches 39; Conservative 27; Mismatches 61; Indels 15; Gaps 5;
QY 59 ILQGSNYSTCAS-CPSCPRMXYGNHCYFVBEKWNSSLEFCLARDSHLLVITDQ 117
DB 156 LTCQLANLKNNGSEVACCPHLWTEHSGSCYFSESEKSWPEADKYCRLENSHLVVVNSLE 215
QY 118 EMSLLQVFLSEAFPCWIGLRNNSG-WRWEDGSP--NFSRISSSFV-----QTCG 164
DB 216 BONFLQNLKLANVSWIGLTDQNGPWRVVDGDFEKGFKNWAPLQPDNWFHGLGGEDCA 275
QY 165 AINKNG-LQASSCEVPLHGVCCK 185
DB 276 HITCGPWNDDVCQTFEVICE 297

RESULT 12

JH0822
Lymphocyte early activation antigen AIM/CD69 - human
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 08-Oct-1999
C:Accession: JH0822; I56167; S60753
R:Lopez-Cabrera, M.; Santis, A.G.; Fernandez-Ruiz, E.; Blacher, R.; Esch, F.; Sanchez-M
J. Exp. Med. 178, 537-547, 1993
A:Title: Molecular cloning, expression, and chromosomal localization of the human earli
mitting receptors.
A:Reference number: JH0822; MUID:93340630; PMID:8340758
A:Accession: JH0822
A:Molecule type: mRNA
A:Residues: 1-199 <LOP>
A:Cross-references: GB:Z22576; NID:g397938; PIDN:CAA80298.1; PID:g397939
A>Note: the authors translated the codon CAA for residue 110 as Glu
R:Hamann, J.; Fiebig, H.; Strauss, M.
J. Immunol. 150, 4920-4927, 1993
A:Title: Expression cloning of the early activation antigen CD69, a type II integral mem
A:Reference number: I56167; MUID:93267093; PMID:8496594
A:Accession: I56167
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-199 <RES>
A:Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1; PID:g291898
R:Santis, A.G.; Lopez-Cabrera, M.; Hamann, J.; Strauss, M.; Sanchez-Madrid, F.

Eur. J. Immunol. 24, 1692-1697, 1994
 A;Title: Structure of the gene coding for the human early lymphocyte activation antigen receptors.

A;Reference number: S60753; MUID:94298875; PMID:8026529
 A;Accession: S60753
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-199 <SAN>
 A;Cross-references: EMBL:Z30426; NID:9525242; PIDN:CAA83017.1; PID:9558352
 C;Comment: This protein is the earliest inducible cell surface glycoprotein expressed in C;Genetics:

A;Gene: GDB:CD69
 A;Cross-references: GDB:132925; OMIM:107273
 A;Map position: 12p13-12p12
 C;Superfamily: C-type lectin homology
 C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
 F;39-64/Domain: transmembrane #status predicted <TM>
 F;88-194/Domain: C-type lectin homology <LCH>
 F;18,30/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F;31/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted
 F;166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.0%; Score 174; DB 2; Length 199;
 Best Local Similarity 22.9%; Pred. No. 5.2e-09;
 Matches 40; Conservative 33; Mismatches 76; Indels 26; Gaps 5;

QY 30 SSKPSCSLVAITLGLTAVLLVLLYCWILCOGSNYSTCASCP-----SC 75
 DB 30 STRHGSFQVPLCAVNVVFIITLITIALISVGQY----NCPQVTFSPSDSHVSSC 85
 QY 76 PDRWMKYGNHCYFVSVEEKDWNSSLEFLCLARDSHLLVITDQMSLLQVFLSEAFWCIGL 135
 DB 86 SEDWVGYORKCYFISTVKRSWTSQAACSEHAGTAVLDSEKDNFKRVAGREHVVGL 145
 QY 136 RNNSG--WRWEDGSPLN--FSRISNSFVOTCGAINKNGIQASCEVPLHGVCKK 186
 DB 146 KKEFGHPKWSNGKEFNWNTGSDK---CVFLKNTVSSMECEKNLYWICNK 196

RESULT 13

JC7608

type II lectin-like immunoreceptor - human

C;Species: Homo sapiens (man)
 C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
 C;Accession: JC7608

R;Huang, X.; Yuan, Z.; Chen, G.; Zhang, M.; Zhang, W.; Yu, Y.; Cao, X.

Biochem. Biophys. Res. Commun. 281, 131-140, 2001

A;Title: Cloning and characterization of a novel ITIM containing lectin-like immunoreceptor
 A;Reference number: JC7608; MUID:21092797; PMID:11178971

A;Contents: Dendritic cells

A;Accession: JC7608

A;Molecule type: mRNA

A;Residues: 1-237 <HUA>

A;Cross-references: GB:AF067800

C;Comment: This receptor, highly homologous to the group of macrophage/hepatic lectins in cell, especially in migrating, antigen capturing and processing.

C;Genetics:

A;Gene: lliir

A;Map position: 12p13

F;45-65/Domain: transmembrane #status predicted <TM>

Query Match 16.5%; Score 169; DB 2; Length 237;
 Best Local Similarity 21.6%; Pred. No. 1.8e-08;
 Matches 52; Conservative 39; Mismatches 92; Indels 58; Gaps 9;

QY 1 MTSVIVYMUEL-----PTAQANDYGPQQSSSKSPSCSLVAITLGLTAVL 50

DB 1 MTSEITYAEVRFKNEFKSGINTASSAASKERTAPLKSNTGFFKLLCASLIIFLLAIS 60

QY 51 LSV-----LLQWILCOGSNY----STCASCPSPDRWMKYGNHCY 87

DB 61 FTIAVIFFOKYSQLEKTKTKELVHTLEVCVKNNFVEETAWSC--CPKNWKSFSNVCY 118

QY 88 YFSVEEKDWNSSLEFLCLARDSHLLVITDQMS--LLQVFLSEAFWCIGLNRNSG---WRW 143
 DB 119 FISTESASWQSEKDCARMEHLLVINTQBEQDFIFQNLQESAYFVGLSDPEGQRHWQ 178
 QY 144 EDGSPFNFSRISSNSF-----VTCGAIN-----KNGLOASSCEVPLHGVCKKVR 188
 DB 179 VDQTPYN-----ESSTFWHPREPSDPNERCVVINFRKPKRWGNDVNCIGPORSVCMMK 234
 QY 189 L 189
 DB 235 I 235

RESULT 14

SI3165

asialoglycoprotein receptor - mouse

N;Alternate names: hepatic lectin

C;Species: Mus musculus (house mouse)

C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999

C;Accession: SI3165

R;Sanford, J.P.; Doyle, D.

Biochim. Biophys. Acta 1087, 259-261, 1990

A;Title: Mouse asialoglycoprotein receptor cDNA sequence: conservation of receptor gene

A;Reference number: SI3165; MUID:91027942; PMID:2223888

A;Accession: SI3165

A;Molecule type: mRNA

A;Residues: 1-301 <SAN>

A;Cross-references: EMBL:X53042; NID:953104; PIDN:CAA37211.1; PID:953105

C;Superfamily: hepatic lectin; C-type lectin homology

C;Keywords: glycoprotein; liver; transmembrane protein

F;170-293/Domain: C-type lectin homology <LCH>

Query Match 16.3%; Score 167; DB 2; Length 301;
 Best Local Similarity 25.9%; Pred. No. 3.6e-08;
 Matches 55; Conservative 29; Mismatches 72; Indels 56; Gaps 9;

QY 27 KSSSSKSPSCSLVAI----TLGLTAVLL-----SVLLY----- 56

DB 92 KETFSNFSSSTLMEFGALDTLGGSTNAITLSWLAQLKEEQQLKADHSTLLFHLKHPMD 151

QY 57 -QWILCO---GSNYSTCASCPSPDRWMKYGNHCYFVSVEEKDWNSSLEFLCLARDSHLL 111

DB 152 LRLTLCQLAYFQNGTEC-----CPNVWVEFGSGCWFSDGLTWAEDQYCOLENAHLL 206

QY 112 VITDQMSLLQVFLSEAFWCIGLNRNSG--WRWEDGSPLNFSRISNSFVQ----- 161

DB 207 VINSREQDFVVKHRQFHIWGLTDRDGSWKWVDGTDYR--SNYRNWAFQPDNMQGHEQ 265

QY 162 ----TCGAINKNG--LQASCEVPLHGVCKKVR 188

DB 266 GGGEDCAEILSDGHNDNFCCQVNRWVCEKRR 297

RESULT 15

T28141

C type lectin, B locus - chicken

C;Species: Gallus gallus (chicken)

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T28141

R;Milne, S.; Kaufman, J.; Beck, S.

submitted to the EMBL Data Library, May 1998

A;Description: DNA sequencing and analysis of the chicken major histocompatibility comp

A;Reference number: Z20475

A;Accession: T28141

A;Status: preliminary; translated from GB/EMBL/DBDJB

A;Molecule type: DNA

A;Residues: 1-156 <ML>

A;Cross-references: EMBL:AL023516; NID:el292539; PID:el292545; PIDN:CAA18961.1

A;Experimental source: clone cB12

C;Genetics:

A;Gene: Blec

A;Map position: 16

A;Introns: 17/1; 74/3; 110/2

Query Match

Best Local Similarity

Matches

46; Conservative

16.2%; Score 166;

DB 2;

Length 156;

29.7%; Pred. No. 2.3e-08;

Mismatches 68;

Indels 22;

Gaps 5;

Qy

42

TLGLTAVLLSVLLYQWILCOGSNYSTCASCPDRCMMKYGNHCYFVSVEEKDWNSSLE

101

Db

6

TVLLITAVAFVQAFQ-----PHPQCAQCPEDWIGFRGKCYFSEDESNTSSQN

56

Qy

102

FCLARDSHLLVITDNQEMSLLOVFLSEAFWIGLRNNS---GWRWEDGSPLNFSRISNS

158

Db

57

NCSALGASLAVFDSAEDLSFTWRHKGSSPHWVGLSREGKEHPWENRSP-----SHL

110

Qy

159

F-VQ---TCGAINKNGLOASSCEVPLHGVCKKVL

189

Db

111

FQVQDGLCAYLGDAGLSSHCSTRNWWCTKPAL

145

Search completed: August 10, 2004, 16:19:35

Job time : 13.0425 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:05:41 ; Search time 7.35929 Seconds
(without alignments)
1337.256 Million cell updates/sec

Title: US-09-811-367B-1

Perfect score: 1023

Sequence: 1 MTDSVIYSMLELPATQAN.....GLQASSCEVPLHGVCVKVRL 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	199	19.5	233	1	1	1	Q95mi5 pan troglod
2	198.5	19.4	179	1	1	1	Q9mkz9 macaca mula
3	196.5	19.2	179	1	1	1	Q13241 homo sapien
4	196.5	19.2	199	1	1	1	CD69 MOUSE
5	194.5	19.0	179	1	1	1	CD94 PANTR
6	191	18.7	227	1	1	1	NK11 MOUSE
7	190	18.6	233	1	1	1	NKGA HUMAN
8	187	18.3	233	1	1	1	NGKC PANTR
9	186	18.2	231	1	1	1	NGKD HUMAN
10	183.5	17.9	216	1	1	1	NGKD MACMU
11	183	17.9	233	1	1	1	NGKD HUMAN
12	180	17.6	216	1	1	1	NGKE HUMAN
13	178.5	17.4	240	1	1	1	NGKE PANTR
14	177.5	17.4	240	1	1	1	NGKE PANTR
15	175.5	17.2	223	1	1	1	NK13 RAT
16	175	17.1	149	1	1	1	CLE2 HUMAN
17	174.5	17.1	304	1	1	1	MMGL MOUSE
18	174	17.0	199	1	1	1	CD69 HUMAN
19	167	16.3	301	1	1	1	LECI MOUSE
20	164.5	16.1	306	1	1	1	MMGL RAT
21	163.5	16.0	283	1	1	1	LECH MOUSE
22	163	15.9	231	1	1	1	NGKC MACMU
23	162	15.8	262	1	1	1	LY4A MOUSE
24	160.5	15.7	223	1	1	1	NK12 MOUSE
25	160.5	15.7	283	1	1	1	LECH RAT
26	157.5	15.4	290	1	1	1	LECH HUMAN
27	156.5	15.3	163	1	1	1	V239 FOWPV
28	156.5	15.3	301	1	1	1	LECI RAT
29	153.5	15.0	167	1	1	1	V008 FOWPV
30	151.5	14.8	283	1	1	1	NK14 MOUSE
31	148.5	14.5	220	1	1	1	KUCR RAT
32	148.5	14.5	550	1	1	1	PBCG MESAU
33	147.5	14.4	175	1	1	1	PBCG MESAU

34	147	14.4	174	1	1	1	PAP3 MOUSE
35	146.5	14.3	548	1	1	1	KUCR MOUSE
36	146	14.3	117	1	1	1	CHBB CROHO
37	146	14.3	311	1	1	1	LECI HUMAN
38	141.5	13.8	1458	1	1	1	PA2R RABIT
39	140.5	13.7	280	1	1	1	KLR7 MOUSE
40	139.5	13.6	3562	1	1	1	PGCV CHICK
41	138.5	13.5	1463	1	1	1	PA2R BOVIN
42	137.5	13.4	175	1	1	1	PAP1 MOUSE
43	137	13.4	165	1	1	1	LITH RAT
44	136.5	13.3	321	1	1	1	PCE2 HUMAN
45	136.5	13.3	331	1	1	1	PCE2 MOUSE

ALIGNMENTS

RESULT 1

NKGA PANTR

ID NKGA PANTR STANDARD; PRT; 233 AA.

AC Q95MI5; Q9MYM6;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE NK2-A/NK2-B type II integral membrane protein (NK2-A/B activating

DE NK receptor) (NK cell receptor A).

GN KRC1 OR NK2A.

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

OX NCBI_TaxID=9598;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20350666; PubMed=10894168;

RA Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,

Muir D.G., Canavez F., Cooper S.I., Valiante N.M., Lanier L.L.,

Parham P.;

RA "Rapid evolution of NK cell receptor systems demonstrated by

RT comparison of chimpanzees and humans."

RL Immunity 12:687-698(2000).

RN [2]

RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND VARIANTS LEU-79 AND

RX ARG-231.

RA MEDLINE=21623889; PubMed=11751968;

RA Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,

Cleland S., Guethlein L.A., Uhrberg M., Parham P.;

RA "Conservation and variation in human and common chimpanzee CD94 and

RT NK2 genes."

RL J. Immunol. 168:240-252(2002).

CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC

CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.

CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.

CC -!- SUBCELLULAR LOCATION: Type II membrane protein.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=NK2-A;

CC IsoId=Q95MI5-1; Sequence=Displayed;

CC Name=NK2-B;

CC IsoId=Q95MI5-2; Sequence=VSP_003066;

CC -!- TISSUE SPECIFICITY: Natural killer cells.

CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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CC or send an email to license@isb-sib.ch).

CC EMBL; AF259055; AAF86965.1; -

DR EMBL; AF259056; AAF86966.1; -

DR EMBL; AF350005; AAK83792.1; -

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DR InterPro: IPR001304; Lectin C.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; FALSE NEG.
DR DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein; Alternative splicing; Polymorphism.
FT DOMAIN 1 70
FT TRANSMEM 71 93
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT CYTOPLASMIC (POTENTIAL)
FT (POTENTIAL).
FT DOMAIN 94 233
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 118 231
FT C-TYPE LECTIN (LONG FORM).
FT DISULFID 119 130
FT BY SIMILARITY.
FT DISULFID 147 229
FT BY SIMILARITY.
FT DISULFID 208 221
FT BY SIMILARITY.
FT CARBOHYD 102 102
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 103 103
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 96 113
FT Missing (in isoform NKG2-B).
FT /FTid=VSP_003066.
FT VARIANT 79 79
FT I -> L (in NKG2-A*03).
FT VARIANT 231 231
FT H -> R (in NKG2-A*03).
SQ SEQUENCE 233 AA; 26212 MW; AE94BEA3A0209984 CRC64;

Query Match 19.5%; Score 199; DB 1; Length 233;
Best Local Similarity 28.4%; Pred. No. 6.7e-12;
Matches 56; Conservative 34; Mismatches 87; Indels 20; Gaps 7;

QY 5 VIYSMLELPTATQ--AQNDYGPQQKSSSKSCSLCAITLGLPAVL---SVLLYQW 58
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 38 ITYAEINLQKASQDPQENDKTYHCKDLPSAP--EKLVGILGIIICLLMASVVTIWI 95
QY 59 ILCQSNYST-----CASCPSPDRMKYGNHCYFSEVKDWNSSLEFCCLARDSHLL 111
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 96 TLIQRHNNSSLNTRTQKARHCHGCPPEWITYNSCYITGKERRTWEESSLACTSKNSGL 155
QY 112 VITDQNSLLQVLEAFQWGL--RNNSGRWEDGSPINFSR--ISSNSFVQTGAINK 168
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 156 SIDNEEMKFLSILSPSS--WLGVPFNSSHHPVVTINGLAFKHEIKDSNAELNCAVLQV 213
QY 169 NGLQASCEVPLHGVCK 185
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 214 NGLKSAQCSSIIYHCK 230

RESULT 2
ID CD94 MACMU STANDARD; PRT; 179 AA.
AC Q9MK9; Q9MK91; Q9MK7; Q9MK8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
DE lectin-like receptor subfamily D, member 1).
GN KLRD1 OR CD94.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20322487; PubMed=10866118;
RA LaBonte M.L., Levy D.B., Letvin N.L.;
RT "Characterization of rhesus monkey CD94/NKG2 family members and
RT identification of novel transmembrane-deleted forms of NKG2-A, B, C,
RT and D.";
RL Immunogenetics 51:496-499(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=21158386; PubMed=11261935;
RA Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.;
RT "Selective expression of NKG2-A and NKG2-C mRNAs and novel alternative

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RT splicing of 5' exons in rhesus monkey decidua."
RL Immunogenetics 53:69-73(2001).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
CC members.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=CD94-A;
CC IsoId=Q9MK9-1; Sequence=Displayed;
CC Name=2; Synonyms=CD94-B;
CC IsoId=Q9MK9-2; Sequence=VSP_003055;
CC Name=3; Synonyms=CD94 alt;
CC IsoId=Q9MK9-3; Sequence=VSP_003054;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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CC -----
CC EMBL; AF190931; AAF74527.1; -
CC EMBL; AF190932; AAF74528.1; -
CC EMBL; AF190933; AAF74529.1; -
CC EMBL; AF294886; AAG34498.1; -
CC HSSP; P22897; LEGG.
CC InterPro: IPR001304; Lectin C.
CC Pfam: PF00059; lectin_c; 1.
CC SMART: SM00034; CLECT; 1.
CC PROSITE; PS00615; C-TYPE_LECTIN_1; FALSE_NEG.
CC PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing; Polymorphism.
FT DOMAIN 1 10
FT CYTOPLASMIC (POTENTIAL).
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT TRANSMEM 11 31
FT (POTENTIAL).
FT DOMAIN 32 179
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 176
FT C-TYPE LECTIN (LONG FORM).
FT DISULFID 61 72
FT BY SIMILARITY.
FT DISULFID 89 174
FT BY SIMILARITY.
FT DISULFID 152 166
FT BY SIMILARITY.
FT CARBOHYD 83 83
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 34
FT MAVFTLWRISGTLGILGICLSMATLGLLKNS -> MAA
FT (in isoform 3).
FT /FTid=VSP_003054.
FT L -> LQ (in isoform 2).
FT /FTid=VSP_003055.
FT Y -> D.
FT VARSPLIC 105 105
FT L -> LQ (in isoform 2).
FT /FTid=VSP_003055.
FT Y -> D.
FT VARIANT 139 139
FT SEQUENCE 179 AA; 20607 MW; 06212B4494527F07 CRC64;
Query Match 19.4%; Score 198.5; DB 1; Length 179;
Best Local Similarity 33.3%; Pred. No. 5.6e-12;
Matches 54; Conservative 24; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCIIVATIGLITAVLLSVLLVQWILCOGSN--YSTCASCSPDRMKYGNHCYFSEV 92
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 20 CLSLMA-TIGILLKNSFTKLSVEPAYTPGNTLEQKDCSCHEKVGRCNCYFISSE 78
QY 93 EKDNWSSLEFCCLARDSHLLVITDQNSLLQVLEAFQWGL---RNNSGRWEDGSP 149
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 79 EXTWNSRHFCASQKSSLLQQRDELDFMS--SQHFYIWIGLSVEEHTAMLENGSAL 136
QY 150 NFSRISSNSF----VQTCGAINKG-LQASSCEVPLHGVCK 186
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 137 --SQYLFTSFETFKPKNCIAVYNSKGNALDESCETKNRYICK 176

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RESULT 3
CD94 HUMAN STANDARD; PRT; 179 AA.
AC Q13241; O43321; O43773; Q9UBB3; Q9UQ00;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
DE lectin-like receptor subfamily D, member 1) (KF43).
GN KLRD1 OR CD94
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=96011848; PubMed=7589107;
RA Chang C., Rodriguez A., Carretero M., Lopez-Botet M., Phillips J.H.,
RA Lanier L.L.;
RA "Molecular characterization of human CD94: a type II membrane
RT glycoprotein related to the C-type lectin superfamily.";
RL Eur. J. Immunol. 25:2433-2437(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=98139529; PubMed=9472066;
RA Rodriguez A., Carretero M., Glienke J., Bellon T., Ramirez A.,
RA Leirach H., Francis F., Lopez-Botet M.;
RA "Structure of the human CD94 C-type lectin gene.";
RL Immunogenetics 47:305-309(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=98267245; PubMed=9601951;
RA Furukawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T., Tadokoro K.,
RA Tohma S., Inoue T., Yamamoto K., Juji T.;
RA "A alternatively spliced form of the human CD94 gene.";
RL Immunogenetics 48:87-88(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
CC members.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;

```

Name=1; Synonyms=CD94-A;
 IsoId=Q13241-1; Sequence=Displayed;
 Name=2; Synonyms=CD94-B;
 IsoId=Q13241-2; Sequence=VSP_003053;
 Name=3; Synonyms=CD94 alt;
 IsoId=Q13241-3; Sequence=VSP_003052;
 -!- TISSUE SPECIFICITY: Natural killer cells.
 -!- SIMILARITY: Contains 1 C-type lectin family domain.
 -!- DATABASE: NAME=PROW; NOTE=CD guide CD94 entry;
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd94.htm".

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EMBL; U30610; AAC50291.1; -;
 EMBL; Y14287; CAA74663.1; -;
 EMBL; Y14288; CAA74663.1; JOINED.
 EMBL; AJ000673; CAA04230.1; -;
 EMBL; AJ000001; CAA03845.1; -;
 EMBL; AB009597; BAA24450.1; -;
 EMBL; AB010084; BAA24451.1; -;
 EMBL; BC028009; AAH28009.1; -;
 PDB; 1B6E; 15-JUN-99.
 Genew; HGNC:6378; KLRD1.
 MIM; 602894; -;
 GO; GO:0005886; C:plasma membrane; TAS.
 GO; GO:0004888; F:transmembrane receptor activity; TAS.
 GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
 GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
 InterPro; IPR001304; Lectin_C.
 Pfam; PF00059; lectin_c; 1.
 SMART; SM00034; CLECT; 1.
 PROSITE; PS00615; C-TYPE LECTIN 1; FALSE NEG.
 PROSITE; PS00041; C-TYPE LECTIN 2; 1.
 KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
 KW Alternative splicing; 3D-structure.
 FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
 FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 98 176 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 61 72 BY SIMILARITY.
 FT DISULFID 89 174 BY SIMILARITY.
 FT DISULFID 152 166 BY SIMILARITY.
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 1 34 MAVKFTLWRLISGTGLICLSIMATGLILKNS -> MAA (in isoform 3).
 FT VARSPLIC 105 105 /FTID=VSP_003052.
 FT VARSPLIC 105 105 L -> IQ (in isoform 2).
 FT SEQUENCE 179 AA; 20497 MW; 1884D99ED9583A7 CRC64;
 SQ

Query Match 19.2%; Score 196.5; DB 1; Length 179;
 Best Local Similarity 32.7%; Pred. No. 8 6e-12;
 Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;
 QY 35 CSCLVAITGLTAVLLSVLLYQWILCOGSN--YSTCASCPCSPDRWMKYGNHYFSVE 92
 DB 20 CLSLMA-TLGIILKNSFTKLSIEPAFTPGNTELQKSDCCSCQEKWVGRCNCFISSE 78
 QY 93 EKDWNSSLEFCLARSHLLVITDNGEMSLQVLFSEAFWIGL---RNNSGWRWDGSL 149
 DB 79 QKTWNESRHLCASQKSSLLQNTDELDFMS--SSQQFYWIGLSYEHTAWLWENGSL 136
 QY 150 NFRSSNSNF----VOTGAINKNG-LQASSCEVPLHGVCCK 186
 DB 137 --SQVLFPSFTFNKNCIAYNPNGNALDESCEDKNRYICKQ 176

DR EMBL; AF259054; AAF86964.1; -;
 DR HSP; P22897; 1EGG.
 DR InterPro; IPR001304; Lectin C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
 DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
 KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
 KW Alternative splicing.
 FT DOMAIN 1 10
 FT TRANSMEM 11 31
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 32 179
 FT DISULFID 98 176
 FT DISULFID 61 72
 FT DISULFID 89 174
 FT DISULFID 152 166
 FT CARBOHYD 83 83
 FT CARBOHYD 132 132
 FT VARSPLIC 105 105
 FT L -> LQ (in isoform 2).
 FT /FTid=VSP_003056.
 SQ SEQUENCE 179 AA; 20493 MW; 7244D99ED9587E7 CRC64;
 Query Match 19.0%; Score 194.5; DB 1; Length 179;
 Best Local Similarity 32.7%; Pred. No. 1.3e-11;
 Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCVAITGLTAVLLSVLLYQWILCOGSN--YSTCASCPCDPKWKYGNHCYFVSVE 92
 Db 20 CLSLMA--TLGILLKNSFTKLSIEFAFTPGNPILQKDSQCEQKWKVGRNCYFISSE 78
 QY 93 EKDNWSSLEFCLARDSHLLVITDQEMSLLOVFLSEAFCLGL--RNNSCWRWEDGSL 149
 Db 79 QKTWNRSHLCASQKSSLLQLQNTDELDFPS--SSQFYWIGLSYSEHTAWLWENGSA 136
 QY 150 NFRSISNSF----VQTGAINKNG-LQASSCEVPLHGVCCK 186
 Db 137 --SQYLPFSFTFNPKNCIAVNPNGNALDESCDKNRYICKQ 176

RESULT 6

NK11_MOUSE
 ID NK11_MOUSE STANDARD; PRT; 227 AA.
 AC P27811;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Natural killer cell surface protein P1-2 (NKR-P1 2) (NKR-P1.7).
 GN KLRB1A OR LY55A OR LY55.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91349596; PubMed=1880421;
 RA Giordano R., Trucco M.;
 RT "Mouse NKR-P1. A family of genes selectively coexpressed in adherent
 RT lymphokine-activated killer cells."
 RL J. Immunol. 147:1701-1708 (1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92013159; PubMed=1680927;
 RA Yokoyama W.M., Ryan J.C., Hunter J.J., Smith H.R.C., Stark M.,
 RA Seaman W.E.;
 RT "cDNA cloning of mouse NKR-P1 and genetic linkage with LY-49.
 RT Identification of a natural killer cell gene complex on mouse
 RT chromosome 6."
 RL J. Immunol. 147:3229-3236 (1991).
 CC -I- FUNCTION: May function as signal-transmitting receptor.
 CC -I- SUBUNIT: Homodimer; disulfide-linked.
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -I- TISSUE SPECIFICITY: Natural killer cells.

CC

CC -I- SIMILARITY: Contains 1 C-type lectin family domain.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; M77676; AAA39822.1; -;
 DR EMBL; M77753; AAA39366.1; -;
 DR PIR; A46467; A46467.
 DR HSP; P22897; 1EGG.
 DR MGD; MGI:107540; Klrbl1a.
 DR InterPro; IPR002353; AntifreezeII.
 DR InterPro; IPR001304; Lectin C.
 DR Pfam; PF00059; lectin_c; 1.
 DR PRINTS; PR00356; ANTI-FREEZEII.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
 DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
 KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
 FT DOMAIN 1 42
 FT TRANSMEM 43 62
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT C-TYPE LECTIN (LONG FORM).
 FT BY SIMILARITY.
 FT DISULFID 94 105
 FT DISULFID 122 210
 FT DISULFID 189 202
 FT CARBOHYD 83 83
 FT CARBOHYD 169 169
 FT CARBOHYD 186 186
 FT CONFLICT 39 39
 FT S -> L (IN REF. 2).
 SQ SEQUENCE 227 AA; 25689 MW; 0599A2587DF0B615 CRC64;
 Query Match 18.7%; Score 191; DB 1; Length 227;
 Best Local Similarity 27.4%; Pred. No. 3.8e-11;
 Matches 49; Conservative 43; Mismatches 71; Indels 16; Gaps 7;

QY 24 PQQSSSSKSCSLVAITGLL-TAVLLSVLLYQ-----WILCOGS-NYST-CASCPS 74
 Db 34 PRSHRSALKSLSCAGLLVLLVTLGMSVLVRLVQKPSIEKCYVLIQENLAKNTDCSAKLE 93
 QY 75 CPDRWMKYNHCYFVSVEEKDNWSSLEFCLARDSHLLVITDQEMSLLOVFLSEAF--CW 132
 Db 94 CPQDWLSHRDKCFHVSQVSNWEEGLVDCGKGATLMLOQDELRLFLDSIKEKNSFW 153
 QY 133 IGLR---NNSGWEDGSPINFS--RISNSFVQTGAINKNGLOASSCEVPLHGVCCK 186
 Db 154 IGLRYTLPMNWKWINGSTLNSDLVKITGTENDSCAAISGDKVTFESCNSDRNWCQK 212

RESULT 7
 NKGA_HUMAN
 ID NKGA_HUMAN STANDARD; PRT; 233 AA.
 AC P26715;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE NK2-A/NKG2-B type II integral membrane protein (NKG2-A/B activating
 DE NK receptor) (NK cell receptor A).
 GN KLRC1 OR NKG2A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS NKG2-A AND NKG2-B).
 RX MEDLINE=91178434; PubMed=2007850;
 RA Houchens J.P., Yabe T., McSherry C., Bach F.H.;
 RT "DNA sequence analysis of NKG2, a family of related cDNA clones


```

FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 2 2 S -> N (in allele NKG2-C*02).
FT VARIANT 102 102 /FTID=VAR_013404.
FT VARIANT 161 161 S -> F (in allele NKG2-C*02).
FT CONFLICT 161 161 M -> I (IN REF. 1).
SQ SEQUENCE 231 AA; 26072 MW; 6B971EECD7542930 CRC64;

Query Match 18.2%; Score 186; DB 1; Length 231;
Best Local Similarity 28.4%; Pred. NO. 1.2e-10;
Matches 48; Conservative 31; Mismatches 76; Indels 14; Gaps 5;

QY 24 PQKSSSSKPCSCCLVAITLGLITAVLLSVLLYQWILCOGQSNYSN----CASCPCSPDRW 79
Db 67 PPEKLTAEVLGIICIV-----LMAFVLKTIIVLIPLEQNNSSPNTRTKARHCHGCPPEW 121
QY 80 MKYGNHCYFVSVEEKDNSSLEFCLARDSHLIVITDQEMSLIQVFLSEAFQWIGL-RNN 138
Db 122 IYNSCYIYIGKERTWESLLACTSKNSLLSIDNEEMKFLASILPSS--WIGVERNS 179
QY 139 SGWRWEDGSPINFSR--ISSNSFVQTGAINKNGLOQSSCEVPLHGVC 185
Db 180 SHHPWVTINGLAFKHKIDSDNAELNCAVLQVNRKLSAQCGSSMIYHCK 228

RESULT 10
NKGD MACMU
ID NKGD MACMU STANDARD; PRT; 216 AA.
AC Q9MZJ7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NKG2-D type II integral membrane protein (NKG2-D activating NK
DE receptor) (NK cell receptor D).
GN NKGD2.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20322487; PubMed=10866118;
RA LaBonte M.L., Levy D.B., Letvin N.L.;
RT "Characterization of rhesus monkey CD94/NKG2 family members and
RT identification of novel transmembrane-deleted forms of NKG2-A, B, C,
RT and D.";
RL Immunogenetics 51:496-499(2000).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
CC EMBL; AF190943; AAF74539.1; -.
CC InterPro; IPR001304; Lectin_C.
CC Pfam; PF00059; lectin_c; 1.
CC SMART; SM00034; CLECT. 1.
CC DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein; Polymorphism.
FT DOMAIN 1 51 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 52 72 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 73 216 (POTENTIAL).
FT DOMAIN 98 213 EXTRACELLULAR (POTENTIAL).
FT DISULFID 99 110 C-TYPE LECTIN (LONG FORM).
FT DISULFID 127 211 BY SIMILARITY.
FT CARBOHYD 115 115 BY SIMILARITY.
FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 216 AA; 25075 MW; A44893F31400DEAC CRC64;

Query Match 17.9%; Score 183.5; DB 1; Length 216;
Best Local Similarity 26.2%; Pred. NO. 1.9e-10;
Matches 49; Conservative 40; Mismatches 75; Indels 23; Gaps 6;

QY 15 ATQANDYGPQOKS-----SSKPCSCCLVAITLG-----LITAVLLSVLLYQWILCO 62
Db 31 STRCQKQPCVIKSKRENASPLFFCCFIAMGIRFIIMVTIWSAVFLNSLFNQEVQIP 90
QY 63 GSNYSTCASCPCSPDRWKMKNHCYFVSVEEKDNSSLEFCLARDSHLIVITDQEMSL 122
Db 91 ----LTSYCGPCPNWICYKNCYQFFNESKNWYESQASCSQNASLLKYSKEDQDL 146
QY 123 QVFLSEAFQWIGL---RNSGWRWEDGSPINFSRISNSFVQTGAINKNGLOA--SSCE 177
Db 147 K--LVKSYHVMGLVHIPNGSWQEDGSLPNLLITTEMQKDCALYASSFKGYIENS 204
QY 178 VPLHGVC 184
Db 205 IPNTYIC 211

RESULT 11
NKGA MACMU
ID NKGA MACMU STANDARD; PRT; 233 AA.
AC Q9MZJ3; Q9MZJ8; Q9MZJ0; Q9MZJ1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NKG2-A/NKG2-B type II integral membrane protein (NKG2-A/B activating
DE NK receptor) (NK cell receptor A).
GN NKGA2.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS NKG2-A; NKG2-ADTM; NKG2-B AND NKG2-BDTM).
RX MEDLINE=20322487; PubMed=10866118;
RA LaBonte M.L., Levy D.B., Letvin N.L.;
RT "Characterization of rhesus monkey CD94/NKG2 family members and
RT identification of novel transmembrane-deleted forms of NKG2-A, B, C,
RT and D.";
RL Immunogenetics 51:496-499(2000).
CC -!- FUNCTION: plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=4;
CC Name=NKG2-A;
CC IsoId=Q9MZJ3-1; Sequence=Displayed;
CC Name=NKG2-B;
CC IsoId=Q9MZJ3-2; Sequence=VSP_003064;
CC Name=NKG2-Adtm;
CC IsoId=Q9MZJ3-3; Sequence=VSP_003063;
CC Name=NKG2-Bdtm;
CC IsoId=Q9MZJ3-4; Sequence=VSP_003065;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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DR EMBL; AF190979; AAF73835.1; -
DR EMBL; AF190981; AAF73837.1; -
DR EMBL; AF190982; AAF73838.1; -
DR EMBL; AF190984; AAF73840.1; -
DR HSP; P22897; IEGG.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLCCT; 1.
DR PROSITE; PS00615; C TYPE LECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C TYPE LECTIN_2; 1.
KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein; Alternative splicing.
FT DOMAIN 1 70
FT TRANSMEM 71 93
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 94 233
FT EXTRACELLULAR (POTENTIAL).
FT C-TYPE LECTIN (LONG FORM).
FT BY SIMILARITY.
FT DISULFID 119 130
FT DISULFID 147 229
FT DISULFID 208 221
FT CARBOHYD 102 102
FT CARBOHYD 103 103
FT CARBOHYD 151 151
FT VARSPPLIC 63 95
FT (in isoform NKG2-Adtm).
FT (FTID=VSP_003063).
FT VARSPPLIC 96 113
FT Missing (in isoform NKG2-B).
FT (FTID=VSP_003064).
FT VARSPPLIC 63 112
FT Missing (in isoform NKG2-Bdtm).
FT (FTID=VSP_003065).
SQ SEQUENCE 233 AA; 26286 MW; 237B2BE36489E76 CRC64;
Query Match 17.9%; Score 183; DB 1; Length 233;
Best Local Similarity 27.5%; Pred. No. 2.3e-10;
Matches 52; Conservative 34; Mismatches 81; Indels 22; Gaps 7;
QY 5 VIYSMLLPATQANDYGPQKSSSKPSCSC---LVAITLGLLTAVLL---SVLLYQ 57
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 38 ITVAELNLQKTSQ---DFQGNKDNHCKDLISAPEKLIAGILGICLVLMASVVTIVIP 94
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 58 WILCOGSNYST-----CASCPCDPWMKYGNHCYFVSVEKDNWSSLEFGLARDSHL 110
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 95 STITQKHNSLSNTRTQKARHCGHCPEWITYNSCYIIGKRRKTWAESLLACTSKNSSL 154
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 111 LVITDQEMSLLOVFLSEAFWIGL-RNNSGWRWEDGSPINFSR--TSSNSFVQTGAIN 167
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 155 LSLDNEEMKFLAILTSS--WIDVFDSSHHPVWTINGLTFRKHEIKESDHAENCAMLH 212
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 168 KNGIQASSC 176
: : : : :
Db 213 VRGLFSDEC 221
: : : : :
RESULT 12
NKG2D HUMAN
ID NKG2D HUMAN STANDARD; PRT; 216 AA.
AC P26716; Q9NR41;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE NKG2-D type II integral membrane protein (NKG2-D activating NK
GN receptor) (NK cell receptor D).
OS Homo sapiens (Human).
```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
RX SEQUENCE FROM N.A.
RA Houchins J.P., Yabe T., McSherry C., Bach P.H.;
RT "DNA sequence analysis of NKG2, a family of human cDNA clones
RT encoding type II integral membrane proteins on human natural killer
RT cells.";
RL J. Exp. Med. 173:1017-1020(1991).
RN [2]
RX SEQUENCE FROM N.A.
RA MEDLINE=98350122; PubMed=9683661;
RA Glienke J., Sobanov Y., Brostjan C., Steffens C., Nguyen C.,
RA Lehrach H., Hofer E., Francis F.;
RT "The genomic organization of NKG2C, E, F, and D receptor genes in the
RT human natural killer gene complex.";
RL Immunogenetics 48:163-173(1998).
RN [3]
RX SEQUENCE FROM N.A.
RA Kothapalli R., Kusmartseva I., Loughran T.P. Jr.;
RT "Identification and characterization of the NKG2D gene from large
RT granular lymphocytic leukemia (LGL) cells.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RX SEQUENCE FROM N.A., AND VARIANT THR-72.
RA MEDLINE=21623889; PubMed=11751968;
RA Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,
RA Cleland S., Guehlein L.A., Uhrberg M., Parham P.;
RT "Conservation and variation in human and common chimpanzee CD94 and
RT NKG2 genes.";
RL J. Immunol. 168:240-252(2002).
RN [5]
RX SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -I- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -I- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
CC -I- SUBCELLULAR LOCATION: Type II membrane protein.
CC -I- TISSUE SPECIFICITY: Natural killer cells.
CC -I- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC EMBL; X54870; CAA38652.1; -
DR Homo sapiens (Human).
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DR EMBL; AJ001687; CAA04925.1; -.
DR EMBL; AJ001688; CAA04925.1; JOINED.
DR EMBL; AJ001689; CAA04925.1; JOINED.
DR EMBL; AF461811; AAL65233.1; -.
DR EMBL; AF260135; AAF86973.1; -.
DR EMBL; AF260136; AAF86974.1; -.
DR EMBL; BC039836; AAK39836.1; -.
DR PIR; PT0375; PT0375.
DR PDB; 1HYR; 23-MAY-01.
DR PDB; 1KCG; 09-JAN-02.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
DR Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein; Polymorphism; 3D-structure.
FT DOMAIN 1 51
FT TRANSMEM 52 72
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 73 216
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 213
FT C-TYPE LECTIN (LONG FORM).
FT DISULFID 99 110
FT BY SIMILARITY.
FT DISULFID 127 211
FT BY SIMILARITY.
FT DISULFID 189 203
FT BY SIMILARITY.
FT CARBOHYD 131 131
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 72 72
FT A -> T (in allele NKG2-D*02).
FT /FTID=VAR 013295.
SQ SEQUENCE 216 AA; 25274 MW; C22F6BD533D7800E CRC64;

Query Match
Best Local Similarity 17.6%; Score 180; DB 1; Length 216;
Matches 42; Conservative 31; Mismatches 52; Indels 32; Gaps 5;

QY 37 CLVAITLG-----LITAVLLSVLLYQWILCOGSNYSTCASCPCDRMKYGNHCY 88
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
57 CFIAVAMGIRFLIMVAWSAVFLNSLFNQEVQIP---LTSYCGPCPKWICYKNKNCVQ 112
QY 89 PSVEKDNSSLEFCLARDSHLLVITDQNSLLQVFLSEAPFCWGL---RNNSCWRWD 145
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
113 PFDESKNYESQASCMSQNASLLKYSKEDQDLK--LVKSYHWMGLVHIPTNGSQWQED 170
QY 146 GSPINFSRI-----SSNSGFVOTCGAIN 167
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
171 GSILSPNLTITMOKGDCALYASSFKGYIENCSTPN 207

RESULT 13
ID NKGE HUMAN STANDARD; PRT; 240 AA.
AC Q07444; Q96RL0; Q9UP04;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NKG2-E type II integral membrane protein (NKG2-E activating NK
DE receptor) (NK cell receptor E).
GN KLRG3 OR NKG2E.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A. (ISOFORM NKG2-E).
RX MEDLINE=94102823; PubMed=8276468;
RA Adamkiewicz T.V., McSherry C., Bach F.H., Houchins J.P.;

"Natural killer lectin-like receptors have divergent carboxy-termini,
distinct from C-type lectins.";
Immunogenetics 39:218-218 (1994).
[2]
RP SEQUENCE FROM N.A. (ISOFORM NKG2-E).
RX MEDLINE=98350122; PubMed=9683661;
RA Glienke J., Sobanov Y., Brostjan C., Steffens C., Nguyen C.,
RA Lehrach H., Hofer E., Francis P.;
"the genomic organization of NKG2C, E, F, and D receptor genes in the
human natural killer gene complex.";
Immunogenetics 48:163-173 (1998).
[3]
RP SEQUENCE FROM N.A. (ISOFORM NKG2-H).
RX MEDLINE=99218418; PubMed=10201920;
RA Bellon T., Heredia A.B., Llano M., Minguella A., Rodriguez A.,
RA Lopez-Botet M., Aparicio P.;
"Triggering of effector functions on a CD8+ T cell clone upon the
aggregation of an activatory CD94/kp39 heterodimer.";
J. Immunol. 162:3996-4002 (1999).
[4]
RP SEQUENCE FROM N.A. (ISOFORM NKG2-E), AND VARIANT ARG-19.
RX MEDLINE=21623889; PubMed=11751968;
RA Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,
RA Cleland S., Guethlein L.A., Uhrberg M., Parham P.;
"Conservation and variation in human and common chimpanzee CD94 and
NK2 genes.";
J. Immunol. 168:240-252 (2002).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=NKG2-E;
IsoId=Q07444-1; Sequence=Displayed;
Name=NKG2-H;
IsoId=Q07444-2; Sequence=VSP 003067;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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-----
EMBL; L14542; AAA16833.1; -.
EMBL; AJ001685; CAA04923.1; -.
EMBL; AF078550; AAD46108.1; -.
EMBL; AF350016; AAK83803.1; -.
EMBL; AF350017; AAK83804.1; -.
PIR; I54524; I54524.
DR HSP; P05451; ILIT.
DR HSP; HGNC:6376; KLRG3.
DR MIM; 602892; -.
DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR GO; GO:0006968; P:cellular defense response; TAS.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
DR Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein; Alternative splicing; Polymorphism.
FT DOMAIN 1 70
FT TRANSMEM 71 93
FT CYTOPLASMIC (POTENTIAL).
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 94 240
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 116 230
FT C-TYPE LECTIN (LONG FORM).
FT DISULFID 117 128
FT BY SIMILARITY.
FT DISULFID 207 220
FT BY SIMILARITY.

```

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FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 227 240 RRGFMILTRVLNS -> VSFRIKALELAVHQIKFYICS
FT NRNDIMIA (in isoform NKG2-H).
FT FTID=VSP 003067.
FT VARIANT 19 19 P -> R (in allele NKG2-B*02).
FT FTID=VAR 013296.
FT VARIANT 135 135 R -> S (in dbSNP:1138437).
FT FTID=VAR 014560.
SQ SEQUENCE 240 AA; 27012 MW; 20691FB21274D8A6 CRC64;
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Query Match 17.4%; Score 178.5; DB 1; Length 240;
Best Local Similarity 28.6%; Pred. No. 6.3e-10;
Matches 46; Conservative 30; Mismatches 70; Indels 15; Gaps 6;

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QY 24 PQQSSSKPSCSCLVAITLGLTAVLLVLLYQWILCOGSNYST----CASCPCPDW 79
DB 67 PPEKLTAEVLGIICIV-----LMAVLKTIVLIPFLEQNNSSPNRTQKARPCGHCPEW 121
QY 80 MKYGNHCYFVSEKDNWNSLFLCLARDSHLLVITDN-QEMSLQVLFSEAFWIGL-RN 137
DB 122 ITYSNSCYITGKERTWEESLQACASKNSSLLSIDNEEMKFLASILPSS--WIGVFN 179
QY 138 NSGWRWEDGSPNFSR--IGSNSFVQTCGAINKNGLOASSC 176
DB 180 SSHHPWTINGLAFKHEIKDSHAERNCAHLVHGLISDQC 220
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RESULT 14
NKGE PANTR STANDARD; PRT; 240 AA.

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AC Q95MT4; Q95MT3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE NKG2-E type II integral membrane protein (NKG2-E activating NK
DE receptor) (NK cell receptor E).
GN KLRC3 OR NKG2E.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT ARG-213.
RX MEDLINE=21623889; PubMed=11751968;
RA Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,
RA Cleland S., Guethlein L.A., Uhrberg M., Parham P.;
RT "Conservation and variation in human and common chimpanzee CD94 and
RT NKG2 genes.";
RL J. Immunol. 168:240-252(2002).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
-----
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-----
DR EMBL; AF350006; AAK83793.1; -
DR EMBL; AF350007; AAK83794.1; -
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein; Polymorphism.
FT DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 93 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 94 240 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 116 230 C-TYPE LECTIN (LONG FORM).
FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 207 220 BY SIMILARITY.
FT VARIANT 213 213 C -> R (IN NKG2-E*02).
SQ SEQUENCE 240 AA; 26996 MW; BC28FB3CEA93A5E0 CRC64;
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Query Match 17.4%; Score 177.5; DB 1; Length 240;
Best Local Similarity 28.0%; Pred. No. 7.9e-10;
Matches 45; Conservative 30; Mismatches 71; Indels 15; Gaps 5;

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QY 24 PQQSSSKPSCSCLVAITLGLTAVLLVLLYQWILCOGSNYST----CASCPCPDW 79
DB 67 PPEKLTAKMLGIICIV-----LMSAVLKTIVLIPFLEQNNSSPNRTQKARPCGHCPEW 121
QY 80 MKYGNHCYFVSEKDNWNSLFLCLARDSHLLVITDN-QEMSLQVLFSEAFWIGLRNN 138
DB 122 ITYSNSCYITGKERTWEESLQACASKNSSLLSIDNEEMKFLASILPSS--WIGVFN 179
QY 139 SG---RWEDGSPNFSRISNSFVQTCGAINKNGLOASSC 176
DB 180 SSHHPWTINGLAFKHEIKDSHAERNCAHLVHGLISDQC 220
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RESULT 15
NK13 RAT STANDARD; PRT; 223 AA.

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AC P27471;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Natural killer cell surface protein P1-3.2.3 (NKR-P1 3.2.3) (Antigen
DE 3.2.3).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90378305; PubMed=2399464;
RA Giorda R., Rudert W.A., Vavassori C., Chambers W.H.,
RA Hiserodt J.C., Trucco M.;
RT "NKR-P1, a signal transduction molecule on natural killer cells.";
RL Science 249:1298-1300(1990).
CC -!- FUNCTION: Mediates transmembrane signaling in natural killer
CC (NK) cells and so may act as a receptor able to selectively
CC trigger NK cell activity.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- MISCELLANEOUS: Ligand binding may be calcium dependent.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
-----
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-----
DR EMBL; M62891; AAA41710.1; -
DR PIR; A35917; A35917.
DR HSP; P22897; 1EGG.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
```

```
DR SMART: SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG.
DR PROSITE; PS0041; C-TYPE LECTIN_2; 1.
KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
FT DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 44 63 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 64 223 (POTENTIAL).
FT DOMAIN 93 212 EXTRACELLULAR (POTENTIAL).
FT DISULFID 94 105 C-TYPE LECTIN (LONG FORM).
FT DISULFID 122 210 BY SIMILARITY.
FT DISULFID 189 202 BY SIMILARITY.
FT CARBOHYD 82 82 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 223 AA; 24551 MW; FCD12B212DDF4330 CRC64;

Query Match 17.2%; Score 175.5; DB 1; Length 223;
Best Local Similarity 27.1%; Pred. No. 1.1e-09;
Matches 49; Conservative 44; Mismatches 67; Indels 21; Gaps 9;

QY 24 PQQKSSSKPSCSLVAITLGLL-TAVLLSVLLYQ-----WILQGSNYSTCASCPS-- 74
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
35 PRSHRLALKSCAGLILVLAIVGMSILVRVLVQPSVEPCRVLIQ-ENLSKTGS-PAKL 92
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : :
75 -CPDRWMKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMSLLOVF---LSEAF 130
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
93 KCPKDWLSHRDKCFHVQSITWKESLADCGKGATLLLVQDQELRFLRNLTKEISSSF 152
QY 131 CWIGLR---NNSGWEDGSPINFs--RISNSFVQTGAINKNGLOASSCEVPLHGVC 185
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
153 -WIGLSYTLSDENWKWINGSTLNSDVLSTGTGTEKDSQSVSDKVLSESCDSDNIVVCQ 211
QY 186 K 186
Db 212 K 212

Search completed: August 10, 2004, 16:16:59
Job time : 8.35929 secs
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:05:01 ; Search time 46.8319 Seconds
(without alignments)
1140.281 Million cell updates/sec

Title: US-09-811-367B-1
Perfect score: 1023
Sequence: 1 MTDVVIYMLELPATQAQN.....GLQASSCEVPLHGVCCKVRL 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	1023	100.0	189	2	AAW88265 Human mas
2	1023	100.0	189	4	AAE11759 Human mas
3	1007	98.4	189	7	ADD25635 Binding d
4	789	77.1	843	4	ABG05451 Novel hum
5	548.5	53.6	188	4	AAE11760 Mouse mas
6	525.5	51.4	188	2	AAAR77033 Mammalian
7	525.5	51.4	188	2	AAW88277 Rat mast
8	525.5	51.4	188	4	AAE11761 Rat mast
9	431	42.1	99	2	AAW88267 Human MAF
10	370.5	36.2	114	2	AAAR77472 Partial s
11	306.5	30.0	70	2	AAW88266 Human MAF
12	230	22.5	231	5	ABBS1897 Human NKp
13	226	22.1	198	4	AAW88815 Human imm
14	226	22.1	198	4	AAU19820 Human nov
15	226	22.1	198	5	ABPA48040 Human pol
16	226	22.1	198	7	ADCI1002 Human pro
17	226	22.1	203	4	AAU19659 Human nov
18	226	22.1	203	5	ABPA47879 Human pol
19	226	22.1	203	7	ADCI10841 Human ext
20	217	21.2	35	4	AAU14192 Peptide #
21	217	21.2	35	4	ABB33139 Peptide #
22	217	21.2	35	4	AAW26602 Peptide #
23	217	21.2	35	4	ABB27967 Human pep
24	217	21.2	35	4	ABB18604 Protein #
25	217	21.2	35	4	AAW66323 Human bon

26	217	21.2	35	4	AAW53935 Human bra
27	217	21.2	35	4	ABG47989 Human liv
28	217	21.2	35	4	AAW01928 Peptide #
29	217	21.2	35	5	ABG35971 Human pep
30	216.5	21.2	182	4	AAU19660 Human nov
31	216.5	21.2	182	5	ABP47880 Human pol
32	216.5	21.2	182	7	ADCI0842 Human ext
33	201	19.6	225	2	AAW65189 Murine mo
34	197	19.3	218	4	AAW64791 Human Kp4
35	196.5	19.2	179	2	AAW40222 CD94. 7/1
36	196.5	19.2	179	2	AAW40222 Human pro
37	196.5	19.2	179	8	ADE76965 Murine CD
38	196.5	19.2	199	2	AAW54660 Mouse CD6
39	196.5	19.2	199	2	AAW85595 O. cunicu
40	195.5	19.1	278	4	AAW5871 NOVX rela
41	194	19.0	268	6	ABJ19328 Human C-t
42	194	19.0	276	6	AAE37769 Chicken 1
43	193	18.9	257	2	AAW85594 Low densi
44	193	18.9	270	2	AAW9586 Low densi
45	193	18.9	270	2	AAW24152 Bovine ID

ALIGNMENTS

RESULT 1
AAW88265
ID AAW88265 standard; protein; 189 AA.

XX AC AAW88265;

XX XX 29-MAR-1999 (first entry)

XX DE Human mast cell function-associated antigen (MAFA).

XX XX Mast cell function-associated antigen; MAFA; splice variant; human;
inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.

XX OS Homo sapiens.

Key	Location/Qualifiers
Peptide	7..10
Modified-site	/note= "ITIM motif"
Modified-site	65..67
Modified-site	/note= "Asn is N-glycosylated"
Modified-site	97..99
Modified-site	/note= "Asn is N-glycosylated"
Modified-site	137..139
Modified-site	/note= "Asn is N-glycosylated"
Modified-site	150..152
Modified-site	/note= "Asn is N-glycosylated"

XX WO9854209-A2.

XX PD 03-DEC-1998.

XX PF 29-MAY-1998; 98WO-GB001572.

XX PR 31-MAY-1997; 97GB-00011148.

XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX PI Hewitt EL, Lamers MBAC, Lamont A, Williams DH;

XX DR WPI; 1999-059806/05.

XX XX N-PSDB; AAW84198.

XX PT New polypeptide having a sequence corresponding to human mast cell
function-associated antigen - useful in forming and manufacturing
pharmaceutical compositions in the treatment of inflammatory and allergic
diseases, and tumour growth.

XX PS Disclosure; Fig 1; 44pp; English.

XX This is the amino acid sequence of human mast cell function- associated
 CC antigen (MAFA), a type II membrane glycoprotein. cDNA (see AAW84198)
 CC encoding human MAFA can be obtained from myelogenous leukaemic cell line
 CC KUB12 or cDNA derived from human lung tissue. The encoded protein is
 CC similar to the rat form (see AAW88277) having an intracellular domain
 CC containing a putative immunoreceptor tyrosine activation motif (ITIM) and
 CC an extracellular lectin-like domain. 2 Alternately spliced forms (see
 CC AAW88266-67) of human MAFA have been identified. Polypeptides and
 CC synthetic peptides (see AAW88258-64) based on these truncated MAFA
 CC proteins can be used in methods for the treatment of inflammatory and
 CC allergic diseases, and tumour growth
 XX Sequence 189 AA;

Query Match 100.0%; Score 1023; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 1.8e-98;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTDSVIYMLPTAQNDYGPQKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
 DB 1 MTDSVIYMLPTAQNDYGPQKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
 QY 61 COGSNYSTCASCPCPDPRWKMKGHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120
 DB 61 COGSNYSTCASCPCPDPRWKMKGHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120
 QY 121 LLQVFLSAFCWIGLRNNSGWRWEDGSPINFSTRSSNSFVOTCGAINKNGLOASCEVPL 180
 DB 121 LLQVFLSAFCWIGLRNNSGWRWEDGSPINFSTRSSNSFVOTCGAINKNGLOASCEVPL 180
 QY 181 HGVCCKVRL 189
 DB 181 HGVCCKVRL 189

RESULT 2

AAE11759
 ID AAE11759 standard; protein; 189 AA.

XX AAE11759;
 AC AAE11759;
 DT 18-DEC-2001 (first entry)
 XX Human mast cell function associated antigen (MAFA) protein.
 DE Human; pharmaceutical composition; mast cell function associated antigen;
 KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
 KW immunosuppressive; cytostatic.
 XX Homo sapiens.
 OS WO200170805-A2.
 XX 27-SEP-2001.
 XX 16-MAR-2001; 2001WO-US008596.
 XX 17-MAR-2000; 2000US-0190716P.
 XX (GEMI-) GEMINI SCI INC.
 XX Takahashi N, Mikayama T;
 XX WPI; 2001-611482/70.
 DR N-PSDB; AAD18734.
 XX Pharmaceutical composition for treating tumor by stimulating cytotoxic
 PT activity of natural killer cell or T-cell, comprises an agent that binds
 PT to mast cell function-associated antigen ligand on target cell.
 XX Claim 10; Page 18; 49pp; English.

CC The present invention relates to a pharmaceutical composition comprising
 CC an agent which specifically binds to a mast cell function associated
 CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
 CC killer (NK)- or T-cell-expressed cell surface MAFA from binding to MAFA
 CC ligand and a pharmaceutically acceptable excipient. The invention is
 CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
 CC binding to a ligand on a target cell, by contacting the pharmaceutical
 CC composition in vitro, ex vivo or in vivo by administering the composition
 CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
 CC on the target cell. The agent or the composition is useful for treating a
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
 CC tumour cell. The invention is also useful for inhibiting an activity of
 CC NK cell or a T-cell. The present sequence is human MAFA protein
 XX

SQ Sequence 189 AA;

Query Match 100.0%; Score 1023; DB 4; Length 189;
 Best Local Similarity 100.0%; Pred. No. 1.8e-98;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTDSVIYMLPTAQNDYGPQKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
 DB 1 MTDSVIYMLPTAQNDYGPQKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
 QY 61 COGSNYSTCASCPCPDPRWKMKGHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120
 DB 61 COGSNYSTCASCPCPDPRWKMKGHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120
 QY 121 LLQVFLSAFCWIGLRNNSGWRWEDGSPINFSTRSSNSFVOTCGAINKNGLOASCEVPL 180
 DB 121 LLQVFLSAFCWIGLRNNSGWRWEDGSPINFSTRSSNSFVOTCGAINKNGLOASCEVPL 180
 QY 181 HGVCCKVRL 189
 DB 181 HGVCCKVRL 189

RESULT 3

ADD25635
 ID ADD25635 standard; protein; 189 AA.

XX ADD25635;
 AC ADD25635;
 DT 15-JAN-2004 (first entry)
 XX Binding domain-immunoglobulin fusion protein-associated protein #95.
 DE Binding domain; immunoglobulin; fusion protein; cytostatic;
 KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
 KW neuroprotective; hinge region; immunoglobulin heavy chain;
 KW CH2 constant region; CH3 constant region; IgG1;
 KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
 KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
 KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
 KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
 XX Unidentified.
 OS US2003118592-A1.
 XX 26-JUN-2003.
 XX 25-JUL-2002; 2002US-00207655.
 XX 17-JAN-2001; 2001US-0367358P.
 PR 17-JAN-2002; 2002US-00053530.
 PR 03-JUN-2002; 2002US-0385691P.
 XX (GENE-) GENE-CRAFT INC.
 XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
 PI

QY 131 CWIGLRNNSGWRWEDGSPLNFSRISSNSFVOTCGAINKN 169
Db 785 CWIGLRNNSGWRWEDGSPLNFSRTNGTIIIRKXHLHKN 823

RESULT 5
ID AAE11760 standard; protein; 188 AA.
XX AAE11760;
XX
DT 18-DEC-2001 (first entry)
XX
DE Mouse mast cell function associated antigen (MAFA) protein.
XX
KW Mouse; pharmaceutical composition; mast cell function associated antigen;
KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
KW immunosuppressive; cytostatic.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Domain 64..188
FT /note= "Extracellular domain"
XX
PN WO200170805-A2.
XX
PD 27-SEP-2001.
XX
PF 16-MAR-2001; 2001WO-US008596.
XX
PR 17-MAR-2000; 2000US-0190716P.
XX
PA (GEMI-) GEMINI SCI INC.
XX
PI Takahashi N, Mikayama T;
DR WPI; 2001-611482/70.
DR N-PSDB; AAD18735.
XX
PT Pharmaceutical composition for treating tumor by stimulating cytotoxic
PT activity of natural killer cell or T-cell, comprises an agent that binds
PT to mast cell function-associated antigen ligand on target cell.
XX
PS Example 1; Page 19; 49pp; English.
XX
CC The present invention relates to a pharmaceutical composition comprising
CC an agent which specifically binds to a mast cell function associated
CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
CC killer (NK) or T-cell-expressed cell surface MAFA from binding to MAFA
CC ligand and a pharmaceutically acceptable excipient. The invention is
CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
CC binding to a ligand on a target cell, by contacting the pharmaceutical
CC composition in vitro, ex vivo or in vivo by administering the composition
CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
CC on the target cell. The agent or the composition is useful for treating a
CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
CC tumour cell. The invention is also useful for inhibiting an activity of
CC NK cell or a T-cell. The present sequence is mouse MAFA protein
XX
SQ Sequence 188 AA;

Query Match 53.6%; Score 548.5; DB 4; Length 188;
Best Local Similarity 55.6%; Pred. No. 6.7e-49;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 MTDSVIYSMLELPTATQNDYGPQOKSSSKPSCSLVAITLGLTAVLLSVLYQWIL 60
Db 1 MADSSIYSTLELPEAPQVDSEKWLKAVLHRPHLSRFANVALGLTIVLMSLLYQRTL 60

QY 131 CWIGLRNNSGWRWEDGSPLNFSRISSNSFVOTCGAINKN 169
Db 785 CWIGLRNNSGWRWEDGSPLNFSRTNGTIIIRKXHLHKN 823

RESULT 6
ID AAR77033 standard; protein; 188 AA.
XX AAR77033;
AC AAR77033;
XX
DT 01-FEB-1996 (first entry)
XX
DE Mammalian mast cell function-associated antigen (MAFA).
XX
KW Mast cell function-associated antigen; MAFA; soluble; ligand;
KW identification; screening; inflammation; inflammatory; allergy; allergic;
KW prevention.
XX
OS Rattus rattus.
XX
PN WO9527734-A1.
XX
PD 19-OCT-1995.
XX
PF 06-APR-1995; 95WO-US004258.
XX
PR 08-APR-1994; 94IL-00109257.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
PA (RYCU/) RYCU A.
XX
PI Pecht I, Guthmann MD, Tal M;
DR WPI; 1995-366356/47.
DR N-PSDB; AAT01471.
XX
PT Novel DNA encoding a mast cell function-associated antigen (MAFA) -
PT useful for screening for ligands of MAFA which are useful for prevention
PT of inflammatory and allergic reactions.
XX
PS Claim 12; Page 37; 54pp; English.
XX
CC A soluble form of mast cell function-associated antigen (MAFA) can be
CC produced by recombinant techniques for use in the ligand- screening
CC assay. The ligands that are identified may be used alone or in
CC combination with the MAFA to prevent inflammatory and allergic reactions
XX
SQ Sequence 188 AA;

Query Match 51.4%; Score 525.5; DB 2; Length 188;
Best Local Similarity 53.5%; Pred. No. 1.7e-46;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MTDSVIYSMLELPTATQNDYGPQOKSSSKPSCSLVAITLGLTAVLLSVLYQWIL 60
Db 1 MADSSIYSTLELPEAPRVQDDSRWKVAVLHRPCVSLVMVALGLTIVLMSLLYQRTL 60

QY 61 CGGSNYSTASCPCSPDRWMKYGNHCYFVSVEEKDWNSLSEFLCLARDSHLLVITDQEMS 120
Db 61 CGSGKGFMCSCQSCPCNLWMRNGSHCYFVSMEKRDWNSLSEFLCLARDSHLLVITDQEMS 120

QY 121 LLOVFLSEAFWCWIGLRNNSGWRWEDGSPLNFSRISSNSFVOTCGAINKNGLQASCEVPL 180
Db 121 LFGYLGQDFYWIGLRNIDGWRWEGPALS-L-RILTNSLIQRCGAHRNGLQASCEVAL 179

QY 181 HGVCCKV 187
Db 180 QWICKV 186

QY 131 CWIGLRNNSGWRWEDGSPLNFSRISSNSFVOTCGAINKN 169
Db 785 CWIGLRNNSGWRWEDGSPLNFSRTNGTIIIRKXHLHKN 823

RESULT 5
ID AAE11760 standard; protein; 188 AA.
XX AAE11760;
XX
DT 18-DEC-2001 (first entry)
XX
DE Mouse mast cell function associated antigen (MAFA) protein.
XX
KW Mouse; pharmaceutical composition; mast cell function associated antigen;
KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
KW immunosuppressive; cytostatic.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Domain 64..188
FT /note= "Extracellular domain"
XX
PN WO200170805-A2.
XX
PD 27-SEP-2001.
XX
PF 16-MAR-2001; 2001WO-US008596.
XX
PR 17-MAR-2000; 2000US-0190716P.
XX
PA (GEMI-) GEMINI SCI INC.
XX
PI Takahashi N, Mikayama T;
DR WPI; 2001-611482/70.
DR N-PSDB; AAD18735.
XX
PT Pharmaceutical composition for treating tumor by stimulating cytotoxic
PT activity of natural killer cell or T-cell, comprises an agent that binds
PT to mast cell function-associated antigen ligand on target cell.
XX
PS Example 1; Page 19; 49pp; English.
XX
CC The present invention relates to a pharmaceutical composition comprising
CC an agent which specifically binds to a mast cell function associated
CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
CC killer (NK) or T-cell-expressed cell surface MAFA from binding to MAFA
CC ligand and a pharmaceutically acceptable excipient. The invention is
CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
CC binding to a ligand on a target cell, by contacting the pharmaceutical
CC composition in vitro, ex vivo or in vivo by administering the composition
CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
CC on the target cell. The agent or the composition is useful for treating a
CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
CC tumour cell. The invention is also useful for inhibiting an activity of
CC NK cell or a T-cell. The present sequence is mouse MAFA protein
XX
SQ Sequence 188 AA;

Query Match 53.6%; Score 548.5; DB 4; Length 188;
Best Local Similarity 55.6%; Pred. No. 6.7e-49;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 MTDSVIYSMLELPTATQNDYGPQOKSSSKPSCSLVAITLGLTAVLLSVLYQWIL 60
Db 1 MADSSIYSTLELPEAPQVDSEKWLKAVLHRPHLSRFANVALGLTIVLMSLLYQRTL 60

QY 131 CWIGLRNNSGWRWEDGSPLNFSRISSNSFVOTCGAINKN 169
Db 785 CWIGLRNNSGWRWEDGSPLNFSRTNGTIIIRKXHLHKN 823

RESULT 6
ID AAR77033 standard; protein; 188 AA.
XX AAR77033;
AC AAR77033;
XX
DT 01-FEB-1996 (first entry)
XX
DE Mammalian mast cell function-associated antigen (MAFA).
XX
KW Mast cell function-associated antigen; MAFA; soluble; ligand;
KW identification; screening; inflammation; inflammatory; allergy; allergic;
KW prevention.
XX
OS Rattus rattus.
XX
PN WO9527734-A1.
XX
PD 19-OCT-1995.
XX
PF 06-APR-1995; 95WO-US004258.
XX
PR 08-APR-1994; 94IL-00109257.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
PA (RYCU/) RYCU A.
XX
PI Pecht I, Guthmann MD, Tal M;
DR WPI; 1995-366356/47.
DR N-PSDB; AAT01471.
XX
PT Novel DNA encoding a mast cell function-associated antigen (MAFA) -
PT useful for screening for ligands of MAFA which are useful for prevention
PT of inflammatory and allergic reactions.
XX
PS Claim 12; Page 37; 54pp; English.
XX
CC A soluble form of mast cell function-associated antigen (MAFA) can be
CC produced by recombinant techniques for use in the ligand- screening
CC assay. The ligands that are identified may be used alone or in
CC combination with the MAFA to prevent inflammatory and allergic reactions
XX
SQ Sequence 188 AA;

Query Match 51.4%; Score 525.5; DB 2; Length 188;
Best Local Similarity 53.5%; Pred. No. 1.7e-46;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MTDSVIYSMLELPTATQNDYGPQOKSSSKPSCSLVAITLGLTAVLLSVLYQWIL 60
Db 1 MADSSIYSTLELPEAPRVQDDSRWKVAVLHRPCVSLVMVALGLTIVLMSLLYQRTL 60

QY 61 CGGSNYSTASCPCSPDRWMKYGNHCYFVSVEEKDWNSLSEFLCLARDSHLLVITDQEMS 120
Db 61 CGSGKGFMCSCQSCPCNLWMRNGSHCYFVSMEKRDWNSLSEFLCLARDSHLLVITDQEMS 120

QY 121 LLOVFLSEAFWCWIGLRNNSGWRWEDGSPLNFSRISSNSFVOTCGAINKNGLQASCEVPL 180
Db 121 LFGYLGQDFYWIGLRNIDGWRWEGPALS-L-RILTNSLIQRCGAHRNGLQASCEVAL 179

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QY 181 HGVCCKV 187
DQ 180 QWICEKV 186

RESULT 7
AAW88277
ID AAW88277 standard; protein; 188 AA.
AC AAW88277;
XX
XX
XX 29-MAR-1999 (first entry)
XX
XX Rat mast cell function-associated antigen (MAFA).
XX Mast cell function-associated antigen; MAFA; splice variant; rat;
XX inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
XX
XX Rattus sp.
XX
XX Key Location/Qualifiers
XX Modified-site 82..84
XX /note= "Asn is N-glycosylated"
XX Modified-site 97..99
XX /note= "Asn is N-glycosylated"
XX
XX WO9854209-A2.
XX
XX 03-DEC-1998.
XX
XX 29-MAY-1998; 98WO-GB001572.
XX
XX 31-MAY-1997; 97GB-00011148.
XX
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
XX
XX WPI; 1999-059806/05.
XX N-PSDB; AAW84222.
XX
XX New polypeptide having a sequence corresponding to human mast cell
XX function-associated antigen - useful in forming and manufacturing
XX pharmaceutical compositions in the treatment of inflammatory and allergic
XX diseases, and tumour growth.
XX
XX Disclosure; Fig 4; 44pp; English.
XX
XX This is the amino acid sequence of rat mast cell function-associated
XX antigen (MAFA), a type II membrane glycoprotein found on mast cells and
XX basophils. The invention relates to cloning of the human MAFA molecule
XX (see AAW88265) and to the discovery of splice variants (see AAW88266-67)
XX of human MAFA that are not found in rat. Polypeptides and synthetic
XX peptides (see AAW88258-64) based on human MAFA and human truncated MAFA,
XX and polynucleotides encoding them, can be used in methods for the
XX treatment of inflammatory and allergic diseases (e.g. rheumatoid
XX arthritis and asthma), and tumour growth
XX
XX Sequence 188 AA;
XX
XX Query Match 51.4%; Score 525.5; DB 2; Length 188;
XX Best Local Similarity 53.5%; Pred. No. 1.7e-46;
XX Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;
XX
QY 1 MTDVSYSMLELPATQAQNDYGPQOKSSSKSCSLVAITGLTLVALLSVLLYQWIL 60
DQ 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRCPCVSLVWVWVGLLTVILMSLLYQRTL 60
XX
QY 61 CQGSNYSTCASCPDRWKYGNHCYFYSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120
DQ 61 CCGSKGFMCSQCRCPLNWRNGSHCYFYSMEKRDWNSSLEKFCADKGSLLTTPDNQGVN 120
XX
QY 121 LLQVFLSEAFWIGIRNNNSGHRWEDGSPFNPSRISSNSFVOTCGAINKNGLOASSCEVPL 180
DQ 121 LFOEYVGEDFYWIGLRDIDGWRWEDGPAISLS-ILSNSVVKQCGTTHRCGLHASSCEVAL 179
XX
QY 181 HGVCCKV 187
DQ 180 QWICEKV 186

RESULT 8
AAE11761
ID AAE11761 standard; protein; 188 AA.
AC AAE11761;
XX
XX 18-DEC-2001 (first entry)
XX
XX Rat mast cell function associated antigen (MAFA) protein.
XX
XX Rat; pharmaceutical composition; mast cell function associated antigen;
XX MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
XX immunosuppressive; cytostatic.
XX
XX Rattus norvegicus.
XX
XX WO200170805-A2.
XX
XX 27-SEP-2001.
XX
XX 16-MAR-2001; 2001WO-US0008596.
XX
XX 17-MAR-2000; 2000US-0190716P.
XX
XX (GEMI-) GEMINI SCI INC.
XX
XX Takahashi N, Mikayama T;
XX
XX WPI; 2001-611482/70.
XX N-PSDB; AAD18736.
XX
XX Pharmaceutical composition for treating tumor by stimulating cytotoxic
XX activity of natural killer cell or T-cell, comprises an agent that binds
XX to mast cell function-associated antigen ligand on target cell.
XX
XX Example 1; Page 19; 49pp; English.
XX
XX The present invention relates to a pharmaceutical composition comprising
XX an agent which specifically binds to a mast cell function associated
XX antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
XX killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
XX ligand and a pharmaceutically acceptable excipient. The invention is
XX useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
XX binding to a ligand on a target cell, by contacting the pharmaceutical
XX composition in vitro, ex vivo or in vivo by administering the composition
XX to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
XX an amount sufficient to inhibit cell surface MAFA binding to the ligand
XX on the target cell. The agent or the composition is useful for treating a
XX tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
XX T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
XX tumour cell. The invention is also useful for inhibiting an activity of
XX NK cell or a T-cell. The present sequence is rat MAFA protein
XX
XX Sequence 188 AA;
XX
XX Query Match 51.4%; Score 525.5; DB 4; Length 188;
XX Best Local Similarity 53.5%; Pred. No. 1.7e-46;
XX Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;
XX
QY 1 MTDVSYSMLELPATQAQNDYGPQOKSSSKSCSLVAITGLTLVALLSVLLYQWIL 60
DQ 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRCPCVSLVWVWVGLLTVILMSLLYQRTL 60
XX
QY 61 CQGSNYSTCASCPDRWKYGNHCYFYSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120
DQ 61 CCGSKGFMCSQCRCPLNWRNGSHCYFYSMEKRDWNSSLEKFCADKGSLLTTPDNQGVN 120
XX

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Db 61 CCGSGKGFMCQSCRCPNLWENGSHCYFSEKRDWNSLKFCAKDGSHLLTFPDNGVN 120
QY 121 LLQVFLSEAFQWIGLRNNSGWRWEDGSPINFSRISNSFVOTCGAINKNGLOASSCEVPL 180
Db 121 LFQEVYVGEDFYWIGLRIDGWRWEDGPALSLS-ILSNSVQKCGTHRCGLHASSCEVAL 179
QY 181 HGVCKKV 187
Db 180 QWICEKV 186

RESULT 9
AAW88267
ID AAW88267 standard; protein; 99 AA.
XX
AC AAW88267;
XX
DT 29-MAR-1999 (first entry)
XX
DE Human MAFA splice variant huMAFA(E3/4-).
XX
KW Mast cell function-associated antigen; MAFA; huMAFA(E3/4-);
KW splice variant; human; inflammation; allergy; asthma;
KW rheumatoid arthritis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9854209-A2.
XX
PD 03-DEC-1998.
XX
PF 29-MAY-1998; 98WO-GB001572.
XX
PR 31-MAY-1997; 97GB-00011148.
XX
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
PI Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
XX
WPI; 1999-059806/05.
DR N-PSDB; AAW84200.
XX
PT New polypeptide having a sequence corresponding to human mast cell
PT function-associated antigen useful in forming and manufacturing
PT pharmaceutical compositions in the treatment of inflammatory and allergic
PT diseases, and tumour growth.
XX
PS Disclosure; Fig 3; 44pp; English.
XX
CC This is the amino acid sequence of human mast cell function- associated
CC antigen (MAFA) splice variant huMAFA(E3/4-), which lacks the C-lectin-
CC like domain of human MAFA (see AAW88265) but retains the intracellular
CC and transmembrane domains as well as the extracellular C-terminal tail.
CC Truncated MAFA polypeptides including huMAFA(E3/4-), and polynucleotides
CC encoding them, as well as synthetic peptides (see AAW88258-64, AAW88268-
CC 72), can be used in compositions for the treatment of
CC inflammatory and allergic diseases (e.g. rheumatoid arthritis and
CC asthma), or tumour growth
XX
SQ Sequence 99 AA;
Query Match 42.1%; Score 431; DB 2; Length 99;
Best Local Similarity 50.3%; Pred. No. 5.4e-37;
Matches 95; Conservative 1; Mismatches 3; Indels 90; Gaps 1;
QY 1 MTDSVIYSMLLELPATQAQNDYGPQKSSSRPSCSLVAITLGLTAVLLSVLLYQWIL 60
Db 1 MTDSVIYSMLLELPATQAQNDYGPQKSSSRPSCSLVAITLGLTAVLLSVLLYQWIL 60
QY 61 CQGSNYSTACSCPSCDPRWKYGNHCYFSEVEKDWNSLSEFCLARDSHLLVITDQMS 120
Db 61 CQG----- 63
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QY 121 LLQVFLSEAFQWIGLRNNSGWRWEDGSPINFSRISNSFVOTCGAINKNGLOASSCEVPL 180
Db 64 -----ISSNSFVOTCGAITKNGLOASSCEVPL 90
QY 181 HGVCKKVRL 189
Db 91 HGWCKKVRL 99

RESULT 10
AAW77472
ID AAW77472 standard; protein; 114 AA.
XX
AC AAW77472;
XX
DT 01-FEB-1996 (first entry)
XX
DE Partial sequence of mast cell function-associated antigen (MAFA).
XX
KW Mast cell function-associated antigen; MAFA; soluble; ligand;
KW identification; screening; inflammation; inflammatory; allergy; allergic;
KW prevention.
XX
OS Rattus rattus.
XX
PN WO9527734-A1.
XX
PD 19-OCT-1995.
XX
PF 06-APR-1995; 95WO-US004258.
XX
PR 08-APR-1994; 94LL-00109257.
XX
PA (YEDA ) YEDA RES & DEV CO LTD.
XX
PA (RYCU/) RYCUS A.
XX
PI Pecht I, Guthmann MD, Tal M;
XX
WPI; 1995-366356/47.
DR N-PSDB; AAT01471.
XX
PT Novel DNA encoding a mast cell function-associated antigen (MAFA) -
PT useful for screening for ligands of MAFA which are useful for prevention
PT of inflammatory and allergic reactions.
XX
PS Disclosure; Page 38; 54pp; English.
XX
CC A soluble form of mast cell function-associated antigen (MAFA) can be
CC produced by recombinant techniques for use in the ligand- screening
CC assay. The ligands that are identified may be used alone or in
CC combination with the MAFA to prevent inflammatory and allergic reactions
XX
SQ Sequence 114 AA;
Query Match 36.2%; Score 370.5; DB 2; Length 114;
Best Local Similarity 58.4%; Pred. No. 1.4e-30;
Matches 66; Conservative 18; Mismatches 28; Indels 1; Gaps 1;
QY 75 CPDRWKYGNHCYFSEVEKDWNSLSEFCLARDSHLLVITDQMSLLOVFLSEAFQWIG 134
Db 1 CPNLWRNGSHCYFSEMEKRDWNSLKFCAKDGSHLLTFPDNGVNLFOEYVYGGDFYWG 60
QY 135 LRNNSGWRWEDGSPINFSRISNSFVOTCGAINKNGLOASSCEVPLHGVCKKV 187
Db 61 LRKIDGWRWEDGPALSLS-ILSNSVQKCGTHRCGLHASSCEVALQWICEKV 112

RESULT 11
AAW88266
ID AAW88266 standard; protein; 70 AA.
XX
AC AAW88266;
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XX 29-MAR-1999 (first entry)
XX Human MAFA splice variant huMAFA(E3-).
XX
XX Mast cell function-associated antigen; MAFA; huMAFA(E3-); splice variant;
XX human; inflammation; allergy; asthma; rheumatoid arthritis; tumour;
XX therapy.
XX
XX Homo sapiens.
XX
XX WO9854209-A2.
XX
XX 03-DEC-1998.
XX
XX 29-MAY-1998; 98WO-GB001572.
XX
XX 31-MAY-1997; 97GB-00011148.
XX
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
XX
XX WPI; 1999-059806/05.
XX
XX N-PSDB; AAV84199.
XX
XX New polypeptide having a sequence corresponding to human mast cell
XX function-associated antigen - useful in forming and manufacturing
XX pharmaceutical compositions in the treatment of inflammatory and allergic
XX diseases, and tumour growth.
XX
XX Disclosure; Fig 2; 44pp; English.
XX
XX This is the amino acid sequence of human mast cell function- associated
XX antigen (MAFA) splice variant huMAFA(E3-). huMAFA(E3-) is a major
XX transcript, not found in rat, but highly expressed in human lung and
XX granulocyte-enriched blood cells. The truncated protein includes the
XX intracellular and transmembrane regions of human MAFA (see AAW88265),
XX followed immediately by a polyproline motif (see AAW88264) due to a
XX reading frameshift. This unique motif has been used to design peptides
XX (see AAW88259-64, AAW88268-72) that inhibit T cell antigen receptor-
XX dependent activation induced by interleukin-2 (IL2) secretion from human
XX Jurkat T cells or IgE dependent degranulation of rat basophil leukaemic
XX cells. Inhibition of IL2 production prevents T cell proliferation and
XX suppresses the immune system. These peptides, truncated MAFA polypeptides
XX including huMAFA(E3-), and polynucleotides encoding them, can be used be
XX used in compositions for the treatment of inflammatory and allergic
XX diseases (e.g. rheumatoid arthritis and asthma), or tumour growth
XX
XX Sequence 70 AA;
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XX Query Match 30.0%; Score 306.5; DB 2; Length 70;
XX Best Local Similarity 82.9%; Pred. No. 3.5e-24;
XX Matches 63; Conservative 1; Mismatches 5; Indels 7; Gaps 1;
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XX 1 MTDVSIYSMLELPATQAQNDYGPQOKSSSRPSCSLVAULTGLLTAVALLSVLLYQWIL 60
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XX 1 MTDVSIYSMLELPATQAQNDYGPQOKSSSRPSCSLVAULTGLLTAVALLSVLLYQWIL 60
XX
XX 61 CQGSNYSTCASCPSCP 76
XX |||||
XX 61 CQ-----EPAPSP 69
XX
XX RESULT 12
XX ABB81897
XX ID ABB81897 standard; protein; 231 AA.
XX
XX AC ABB81897;
XX
XX 03-OCT-2002 (first entry)
XX
XX Human NKp80.

```

```

XX Human; NKp80; triggering NK; lymphoproliferative diseases; LDGL;
XX lymphocyte.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 24 /note= "Encoded by CAA"
XX Misc-difference 43 /note= "Encoded by ACA"
XX Misc-difference 64 /note= "Encoded by CAG"
XX Misc-difference 158 /note= "Encoded by ATC"
XX
XX EP1219637-A1.
XX
XX 03-JUL-2002.
XX
XX 27-DEC-2000; 2000EP-00403689.
XX
XX 27-DEC-2000; 2000EP-00403689.
XX
XX (INNA-) INNATE PHARMA.
XX (UYGE-) UNIV GENOVA.
XX
XX Moretta A, Bottino C, Biassoni R;
XX
XX WPI; 2002-521944/56.
XX N-PSDB; ABQ78832.
XX
XX New NKp80 polypeptides having a triggering NK activity, useful as markers
XX for typing lymphoproliferative diseases of granular lymphocytes, or for
XX identifying abnormal cells in the whole lymphocyte population in patient.
XX
XX Claim 4; SEQ ID NO 1; 21pp; English.
XX
XX The invention relates to a novel human polypeptide (designated NKp80)
XX having a triggering NK activity, or its immunogenic fragments. The NKp80
XX polypeptide is useful as NK cell markers, as markers for typing
XX lymphoproliferative diseases of granular lymphocytes (LDGL), or for
XX identifying abnormal cells in the whole lymphocyte population of the
XX patient. The antibodies against these polypeptides are useful for
XX inhibiting NK cell cytotoxicity or NK cell depletion. The sequence
XX represents the human NKp80 polypeptide of the invention. N.B. The
XX sequence data for this patent is not represented in the printed
XX specification, but is based on sequence information supplied by the
XX European Patent Office
XX
XX Sequence 231 AA;
XX
XX Query Match 22.5%; Score 230; DB 5; Length 231;
XX Best Local Similarity 28.6%; Pred. No. 1.7e-15;
XX Matches 63; Conservative 32; Mismatches 61; Indels 64; Gaps 9;
XX
XX 26 QKSSSKPSCSL--VAITL-----GLLTAVLLSVLLY-----QWILCQ3-- 63
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 15 KRSSAQTSCLTFKDYSVTLHWYKILLIGISGTVNGIITLTLISLLIVSCGVLLKCKQGS 74
XX
XX 64 -----SNYSTCASCPS-----CPDRMKYGNHCYFVSVEKD 95
XX ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 75 CSNATQVEDTGLKVNNGTFRNINSDLCASRSADQTVLCQSEWLKYQKCYWFSNEMKS 134
XX
XX 96 WNSSLBFLCLARDSHLLVITDNOQMSLLQVFLSEA-FCWIGLRNNS---GWRWEDGSPLN 151
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 135 WSDSYVYVCLERKSHLLIIHDQLEWAFIQKNLRQLNVYVWIGLNTSLKMTWTWVGSPID- 193
XX
XX 152 SRISNSFWO-----TCGAINKNGLOASSCEVPLHGVCX 185
XX ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 194 ---SKIFFIKGPAKENSAAIKESKIFSETCSSVFKWICQ 230
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RESULT 13
AAM88815
ID AAM88815 standard; protein; 198 AA.
XX
AC AAM88815;
XX
DT 07-NOV-2001 (first entry)
XX
XX Human immune/haematopoietic antigen SEQ ID NO:16408.
DE
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytotaxtic; gene therapy; vaccine; metastasis.
KW
OS Homo sapiens.
XX
XX WO200157182-A2.
PN
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
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PR 12-SEP-2000; 2000US-0231968P.
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	XX		
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	XX	Human polypeptide SEQ ID NO 470.	
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	XX		
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XX	OS	Homo sapiens.	
XX	XX		
PN	PX	US2002042386-A1.	
XX	XX		
PD	PF	11-APR-2002.	
XX	PP		
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:18:53 ; Search time 40.4761 Seconds
(without alignments)
1464.718 Million cell updates/sec

Title: US-09-811-367B-1

Perfect score: 1023

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Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1007	98.4	189	14 US-10-207-655-196	Sequence 196, App
3	548.5	53.6	188	9 US-09-811-367B-3	Sequence 3, Appli
4	525.5	51.4	188	9 US-09-811-367B-5	Sequence 5, Appli
5	230	22.5	231	16 US-10-451-843-1	Sequence 1, Appli
6	226	22.1	198	9 US-09-764-870-470	Sequence 470, App
7	226	22.1	198	14 US-10-125-540-470	Sequence 470, App
8	226	22.1	203	9 US-09-764-870-309	Sequence 309, App
9	226	22.1	203	14 US-10-125-540-309	Sequence 309, App
10	217	21.2	35	9 US-09-864-761-33902	Sequence 33902, A
11	216.5	21.2	182	9 US-09-764-870-310	Sequence 310, App
12	216.5	21.2	182	14 US-10-125-540-310	Sequence 310, App
13	201	19.6	225	15 US-10-379-127-25	Sequence 25, Appl
14	196.5	19.2	179	10 US-09-919-039-130	Sequence 130, App
15	196.5	19.2	179	15 US-10-335-009-10	Sequence 10, Appl

16	196.5	19.2	199	14	US-10-179-528-7	Sequence 7, Appli
17	195.5	19.1	278	14	US-10-220-511-11	Sequence 11, Appl
18	194	19.0	268	15	US-10-161-493-22	Sequence 22, Appl
19	193.5	18.9	226	14	US-10-002-631C-295	Sequence 295, App
20	193	18.9	257	14	US-10-179-528-4	Sequence 4, Appli
21	193	18.9	270	14	US-10-220-511-4	Sequence 4, Appli
22	190	18.6	265	9	US-09-764-870-307	Sequence 307, App
23	190	18.6	265	14	US-10-125-540-307	Sequence 307, App
24	189.5	18.5	275	15	US-10-161-493-20	Sequence 20, Appl
25	187	18.3	399	16	US-10-451-459-2	Sequence 2, Appli
26	185.5	18.1	316	9	US-09-862-802-4	Sequence 4, Appli
27	183	17.9	319	15	US-10-138-588-90	Sequence 90, Appl
28	182	17.8	216	15	US-10-335-009-8	Sequence 8, Appli
29	181	17.7	273	9	US-09-796-858-47	Sequence 47, Appl
30	181	17.7	273	14	US-10-220-511-2	Sequence 2, Appli
31	180.5	17.6	546	12	US-10-072-012-158	Sequence 158, App
32	180.5	17.6	549	12	US-10-072-012-160	Sequence 160, App
33	180	17.6	223	12	US-10-276-774-2216	Sequence 2216, Ap
34	179.5	17.5	273	9	US-09-862-802-10	Sequence 10, Appl
35	179	17.5	267	15	US-10-138-588-88	Sequence 88, Appl
36	178	17.4	345	12	US-10-262-839-94	Sequence 94, Appl
37	176	17.2	404	10	US-09-891-894-1	Sequence 1, Appli
38	176	17.2	404	12	US-10-151-274-2	Sequence 2, Appli
39	176	17.2	404	14	US-10-184-150-1	Sequence 1, Appli
40	176	17.2	404	15	US-10-369-214-131	Sequence 131, App
41	176	17.2	404	15	US-10-328-997-1	Sequence 1, Appli
42	175	17.1	149	10	US-09-284-320-11	Sequence 11, Appl
43	175	17.1	149	13	US-10-114-893-32	Sequence 32, Appl
44	175	17.1	149	14	US-10-088-859-2	Sequence 2, Appli
45	175	17.1	149	14	US-10-179-528-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-811-367B-1
; Sequence 1, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No, US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-811-367B-1

Query Match 100.0%; Score 1023; DB 9; Length 189;
Best Local Similarity 100.0%; Pred.No 3.5e-97;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTDSVIYSMLLPATQAQNDYGPQQKSSKSPSCSCLVAITLGLLTAVLLSVLLQWIL 60
DB	1	MTDSVIYSMLLPATQAQNDYGPQQKSSKSPSCSCLVAITLGLLTAVLLSVLLQWIL 60
QY	61	CQGSNVTSCASCPDPRWKYGNHCYFVSVEKDNSSLEFCLARDSHLLVITDQEMS 120
DB	61	CQGSNVTSCASCPDPRWKYGNHCYFVSVEKDNSSLEFCLARDSHLLVITDQEMS 120
QY	121	LLOQVFLSEAFCTWGLRNNSWEDGSPNFRISNSFVQTGATKNGKQASSCEVPL 180
DB	121	LLOQVFLSEAFCTWGLRNNSWEDGSPNFRISNSFVQTGATKNGKQASSCEVPL 180

Qy 181 HGVCCKVRL 189
Db 181 HGVCCKVRL 189

RESULT 2
US-10-207-655-196
; Sequence 196 Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 196
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-196

Query Match 98.4%; Score 1007; DB 14; Length 189;
Best Local Similarity 98.4%; Pred. No. 1.6e-95;
Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MTDSVIYSMLELPTATQANDYGPQKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
Db 1 MTDSVIYSMLELPTATQANDYGPQKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60

Qy 61 CQGSNYSTCASCPCPDPRMVKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
Db 61 CQGSNYSTCASCPCPDPRMVKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120

Qy 121 LLOVFLSEAFWCWIGLRNNSGWRWEDGSPINFSRISNSSNFVOTCGAINKNGLOASSCEVPL 180
Db 121 LLOVFLSEAFWCWIGLRNNSGWRWEDGSPINFSRISNSSNFVOTCGAINKNGLOASSCEVPL 180

Qy 181 HGVCCKVRL 189
Db 181 HWVCCKVRL 189

RESULT 3
US-09-811-367B-3
; Sequence 3, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-811-367B-3

Query Match 53.6%; Score 548.5; DB 9; Length 188;
Best Local Similarity 55.6%; Pred. No. 2.9e-48;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

Qy 1 MTDSVIYSMLELPTATQANDYGPQKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
Db 1 MADSSYISTLELPEAPQVQDESRLKAVLHRLPHLSRFAMVALGLTTLVILSLMYQRI 60

Qy 61 CQGSNYSTCASCPCPDPRMVKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
Db 61 CQGSNYSTCASCPCPDPRMVKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120

Qy 121 LLOVFLSEAFWCWIGLRNNSGWRWEDGSPINFSRISNSSNFVOTCGAINKNGLOASSCEVPL 180
Db 121 LLOVFLSEAFWCWIGLRNNSGWRWEDGSPINFSRISNSSNFVOTCGAINKNGLOASSCEVPL 180

Qy 181 HGVCCKV 187
Db 180 QWICKV 186

RESULT 4
US-09-811-367B-5
; Sequence 5, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-811-367B-5

Query Match 51.4%; Score 525.5; DB 9; Length 188;
Best Local Similarity 53.5%; Pred. No. 6.7e-46;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

Qy 1 MTDSVIYSMLELPTATQANDYGPQKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
Db 1 MADNSIYSTLELPEAPRVQDDSRWKVAVLHRLPHLSRFAMVALGLTTLVILSLMYQRI 60

Qy 61 CQGSNYSTCASCPCPDPRMVKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
Db 61 CQGSNYSTCASCPCPDPRMVKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120

Qy 121 LLOVFLSEAFWCWIGLRNNSGWRWEDGSPINFSRISNSSNFVOTCGAINKNGLOASSCEVPL 180
Db 121 LLOVFLSEAFWCWIGLRNNSGWRWEDGSPINFSRISNSSNFVOTCGAINKNGLOASSCEVPL 180

Qy 181 HGVCCKV 187
Db 180 QWICKV 186

RESULT 5
US-10-451-843-1
; Sequence 1, Application US/10451843
; Publication No. US20040115738A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; APPLICANT: UNIVERSITA DI GENOVA
; TITLE OF INVENTION: Polypeptides having a triggering NK receptor activity and biolog
; FILE REFERENCE: 1249NKP80
; CURRENT APPLICATION NUMBER: US/10/451,843
; CURRENT FILING DATE: 2003-12-30

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; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-451-843-1

Query Match      22.5%; Score 230; DB 16; Length 231;
Best Local Similarity 28.6%; Pred. No. 2.5e-15;
Matches 63; Conservative 32; Mismatches 61; Indels 64; Gaps 9;

QY 26 QKSSSPKSCSL--VAITL-----GLLTAVLLSVLLY---QWTLCOG-- 63
Db 15 KKRSSAGTCLTFKDYGVTHWYKILLIGISGTWNGILTLISLILVSGVLLKQKGS 74
QY 64 -----SNYSTCASCPS-----CPDRMKYGNHCYFFSVEEKD 95
Db 75 CSNATQYEDTGLKVNNGTRRNISNKDLCASRSADQTVLCQSEWLKYQKCYFNSNEMKS 134
QY 96 WNSLEFLCLARDSHLLVITDQEMSLLOVFLSEA-FCWIGLRNNS-----GWRWEDGSPINF 151
Db 135 WSDSYVYCLERKSHLLIHDQLEMAFIQKNLRQLNLYWVIGLFTSLKMTWTWVDGSPID- 193
QY 152 SRISNSFVQ-----TCGAINKNGLOASSCEVPLHGVCV 185
Db 194 ---SKIFFIKGPAKENSAAIKESKIFSETCSSVFKWICQ 230

RESULT 6
US-09-764-870-470
; Sequence 470, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14
; CURRENT APPLICATION NUMBER: US/09/764,870
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 470
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-470

Query Match      22.1%; Score 226; DB 9; Length 198;
Best Local Similarity 31.2%; Pred. No. 5.4e-15;
Matches 58; Conservative 27; Mismatches 53; Indels 48; Gaps 8;

QY 44 GLLTAVLLSVLLY--QWIL--COG-----SNYSTCASCPS 74
Db 16 GILTLTILSLILVSGVLLKQKGCSCSNATQYEDTGLKVNNGTRRNISNKDLCASRSA 75
QY 75 -----CPDRMKYGNHCYFFSVEEKDWSLEFLCLARDSHLLVITDQEMSLLOVFLSEA 129
Db 76 DQTVLCQSEWLKYQKCYFNSNEMKSWSDSYVYCLERKSHLLIHDQLEMAFIQKNLRQL 135
QY 130 -FCWIGLRNNS---GWRWEDGSPINFSRISNSFVQ-----TCGAINKNGLOASSCEVP 179
Db 136 NYVMVIGLFTSLKMTWTWVDGSPID---SKIFFIKGPAKENSAAIKESKIFSETCSSV 191
QY 180 LHGVCK 185
Db 192 FKWICQ 197

RESULT 8
US-09-764-870-309
; Sequence 309, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14
; CURRENT APPLICATION NUMBER: US/09/764,870
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 309
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-309

Query Match      22.1%; Score 226; DB 9; Length 203;
Best Local Similarity 31.2%; Pred. No. 5.5e-15;
Matches 58; Conservative 27; Mismatches 53; Indels 48; Gaps 8;

QY 44 GLLTAVLLSVLLY--QWIL--COG-----SNYSTCASCPS 74
Db 21 GILTLTILSLILVSGVLLKQKGCSCSNATQYEDTGLKVNNGTRRNISNKDLCASRSA 80
QY 75 -----CPDRMKYGNHCYFFSVEEKDWSLEFLCLARDSHLLVITDQEMSLLOVFLSEA 129
Db 81 DQTVLCQSEWLKYQKCYFNSNEMKSWSDSYVYCLERKSHLLIHDQLEMAFIQKNLRQL 140
QY 130 -FCWIGLRNNS---GWRWEDGSPINFSRISNSFVQ-----TCGAINKNGLOASSCEVP 179
Db 141 NYVMVIGLFTSLKMTWTWVDGSPID---SKIFFIKGPAKENSAAIKESKIFSETCSSV 196
QY 180 LHGVCK 185
Db 192 FKWICQ 197

RESULT 7
US-10-125-540-470
; Sequence 470, Application US/10125540
; Publication No. US20030059875A1
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; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US 09/475,365
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 10
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-009-10

Query Match      19.2%; Score 196.5; DB 15; Length 179;
Best Local Similarity 32.7%; Pred. No. 5.2e-12;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

Qy      35 CSCLVAITLGLLTAVLLSVLLYQWILCOGSN--YSTCASCPCSPDRWKKYGNHCYFVSVE 92
Db      20 CLSLMA-TIGILLKNSFTKLSIEPAFTGPNIELQKDSCCQEKWGYRCNCYFISSE 78
Qy      93 EKDNSSLEFCLARDSHLLVITDNOEMSLIQVFLSEAFCWIGL--RNNSGMRWEDGSPL 149
Db      79 QKTWNEERHLCAQKSSLLQONTDELDFMS--SSQQFYWIGLSYSEHTAWLWENGSA 136
Qy      150 NFSRISSNSF----VQTGAINKNG-LQASCEVELHGVCKK 186
Db      137 --SOVLPPSFETFKNCIAYNPNGNALDESCDKNRYICKQ 176
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Search completed: August 10, 2004, 16:32:36
Job time : 41.4761 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:13:57 ; Search time 14.7186 Seconds
(without alignments)
662.924 Million cell updates/sec

Title: US-09-811-367B-1
Perfect score: 1023
Sequence: 1 MTDSVIYSMLELPTAQQN.....GLQASCEVPLHGVCCKVRL 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	525.5	51.4	188	3	US-08-722-126A-5
2	525.5	51.4	188	5	PCT-US95-04258-5
3	430	42.0	76	4	US-09-531-056A-23
4	370.5	36.2	114	3	US-08-722-126A-6
5	370.5	36.2	114	5	PCT-US95-04258-6
6	201	19.6	225	2	US-08-738-462-2
7	201	19.6	225	5	PCT-US94-07587-2
8	196.5	19.2	179	1	US-08-690-095-9
9	196.5	19.2	179	2	US-08-650-578-2
10	196.5	19.2	179	2	US-08-688-342-3
11	196.5	19.2	179	2	US-09-113-788-3
12	196.5	19.2	179	3	US-09-113-789-9
13	196.5	19.2	199	5	PCT-US93-10418-4
14	193	18.9	270	2	US-09-055-095-4
15	193	18.9	270	2	US-08-809-494A-2
16	193	18.9	270	3	US-09-352-302-2
17	193	18.9	273	2	US-08-809-494A-4
18	193	18.9	273	3	US-09-352-302-4
19	190	18.6	233	1	US-08-690-095-8
20	190	18.6	233	3	US-09-113-789-8
21	190	18.6	233	3	US-08-543-246B-2
22	190	18.6	233	3	US-08-543-246B-21
23	185.5	18.1	316	3	US-09-111-470-4
24	184	18.0	215	1	US-08-690-095-7
25	184	18.0	215	3	US-09-113-789-7
26	184	18.0	215	3	US-08-543-246B-16
27	184	18.0	215	3	US-08-543-246B-22

28	182	17.8	231	1	US-08-690-095-6	Sequence 6, Appli
29	182	17.8	231	3	US-09-113-789-6	Sequence 6, Appli
30	182	17.8	231	3	US-08-543-246B-6	Sequence 6, Appli
31	182	17.8	231	3	US-08-543-246B-23	Sequence 23, Appli
32	181	17.7	273	2	US-09-055-095-3	Sequence 3, Appli
33	181	17.7	273	2	US-08-809-494A-6	Sequence 6, Appli
34	181	17.7	273	3	US-09-352-302-6	Sequence 6, Appli
35	180	17.6	216	3	US-08-543-246B-9	Sequence 9, Appli
36	180	17.6	216	3	US-08-543-246B-24	Sequence 24, Appli
37	179.5	17.5	273	3	US-09-111-470-10	Sequence 10, Appli
38	179.5	17.5	292	2	US-08-688-342-4	Sequence 4, Appli
39	179.5	17.5	292	2	US-09-113-788-4	Sequence 4, Appli
40	176	17.2	404	4	US-09-517-605-2	Sequence 2, Appli
41	175.5	17.2	168	3	US-08-772-440-17	Sequence 17, Appli
42	175.5	17.2	201	2	US-08-688-342-1	Sequence 1, Appli
43	175.5	17.2	201	2	US-09-113-788-1	Sequence 1, Appli
44	174	17.0	199	5	PCT-US93-10418-2	Sequence 2, Appli
45	173	16.9	175	3	US-08-772-440-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1
US-08-722-126A-5
; Sequence 5, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-722-126A-5

Query Match 51.4%; Score 525.5; DB 3; Length 188;
Best Local Similarity 53.5%; Pred. No. 1.1e-48;

Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;
QY 1 MTDSVIYMLELPTAQNDYGPQOKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
Db 1 MADNSIYSTLELPAAPRVQDDSRWKAVLHPCVSYLVMMVALGLTITVILMSLLDYQRTL 60
QY 61 CQGSNYSTCASCPCPDWRMKYGNHCYFVSVEEKDWNSSLFCLARDSHLLVITDQEMS 120
Db 61 CCGSGKGFMCQSCRCPLWNRNGSHCYFVSMEKRDWNSLKFCDKDGSHLLTFFPDQGVN 120
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Db 121 LFQEVYGVDFYIGLRIDGWRWEDGPALSLS-ILSNSVWQKGTIHRCGLHASCEVAL 179
QY 181 HGVCKKV 187
Db 180 QWICEKV 186

RESULT 2
PCT-US95-04258-5
; Sequence 5, Application PC/TUS9504258
; GENERAL INFORMATION:
; APPLICANT: BROWDY AND NEIMARK
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04258-5

Query Match 51.4%; Score 525.5; DB 5; Length 188;
Best Local Similarity 53.5%; Pred. No. 1.1e-48;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;
QY 1 MTDSVIYMLELPTAQNDYGPQOKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
Db 1 MADNSIYSTLELPAAPRVQDDSRWKAVLHPCVSYLVMMVALGLTITVILMSLLDYQRTL 60
QY 61 CQGSNYSTCASCPCPDWRMKYGNHCYFVSVEEKDWNSSLFCLARDSHLLVITDQEMS 120
Db 61 CCGSGKGFMCQSCRCPLWNRNGSHCYFVSMEKRDWNSLKFCDKDGSHLLTFFPDQGVN 120

QY 121 LLQVFLSEAPCWIGLRNNSGWRWEDGSPINFSRISNSSNFVQTCGAINKNGLOASCEVPL 180
Db 121 LFQEVYGVDFYIGLRIDGWRWEDGPALSLS-ILSNSVWQKGTIHRCGLHASCEVAL 179
QY 181 HGVCKKV 187
Db 180 QWICEKV 186
RESULT 3
US-09-531-056A-23
; Sequence 23, Application US/09531056A
; Patent No. 6455683
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUS
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531.056A
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-531-056A-23
Query Match 42.0%; Score 430; DB 4; Length 76;
Best Local Similarity 98.7%; Pred. No. 6e-39;
Matches 75; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 73 PSCPDWRMKYGNHCYFVSVEEKDWNSSLFCLARDSHLLVITDQEMSLLQVFLSEAFCW 132
Db 1 PSCPDWRMKYGNHCYFVSVEEKDWNSSLFCLARDSHLLVITDQEMSLLQVFLSEAFCW 60
QY 133 IGLRNSGWRWEDGSP 148
Db 61 IGLRNSGWRWEDGSP 76

RESULT 4
US-08-722-126A-6
; Sequence 6, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722.126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257

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; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PCHT=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-722-126A-6

Query Match 36.2%; Score 370.5; DB 3; Length 114;
Best Local Similarity 58.4%; Pred. No. 2.6e-32;
Matches 66; Conservative 18; Mismatches 28; Indels 1; Gaps 1;

QY 75 CPDRWMKYGNHCYFYSVEEKDWNSSLEFCLARDSHLLVITDQMSLLQVFLSEAFQWIG 134
Db 1 CPNLWMNGSCHYFYSMEKEDWNSLKFCAKDGSHLLTFDPDQGVNLFQEVVGDFFWIG 60

QY 135 LRNSGWRWEDGSPNFSRISNSFVQTCGAINKNGLOASSCEVPLHGVCCKV 187
Db 61 LRIDGWRWEDGPALSLS-ILNSNVQKGTIHRGGLHASSCEVALQWICEKV 112

RESULT 5
PCT-US95-04258-6
; Sequence 6, Application PC/TUS9504258
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IEM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PCHT=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-04258-6

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Query Match 36.2%; Score 370.5; DB 5; Length 114;
Best Local Similarity 58.4%; Pred. No. 2.6e-32;
Matches 66; Conservative 18; Mismatches 28; Indels 1; Gaps 1;

QY 75 CPDRWMKYGNHCYFYSVEEKDWNSSLEFCLARDSHLLVITDQMSLLQVFLSEAFQWIG 134
Db 1 CPNLWMNGSCHYFYSMEKEDWNSLKFCAKDGSHLLTFDPDQGVNLFQEVVGDFFWIG 60

QY 135 LRNSGWRWEDGSPNFSRISNSFVQTCGAINKNGLOASSCEVPLHGVCCKV 187
Db 61 LRIDGWRWEDGPALSLS-ILNSNVQKGTIHRGGLHASSCEVALQWICEKV 112

RESULT 6
US-08-738-462-2
; Sequence 2, Application US/08738462
; Patent No. 5965401
; GENERAL INFORMATION:
; APPLICANT: Chang, Chiwen
; APPLICANT: Lanier, Lewis L.
; APPLICANT: Phillips Jr., Joseph H.
; TITLE OF INVENTION: Purified Mammalian NK Antigens and
; RELATED REAGENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IEM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/738,462
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,435
; FILING DATE: 16-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Chang, Egwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0397
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-738-462-2

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Query Match 19.6%; Score 201; DB 2; Length 225;
Best Local Similarity 26.0%; Pred. No. 1.1e-13;
Matches 58; Conservative 36; Mismatches 81; Indels 48; Gaps 8;

QY 1 MTDSVIYMLELPTAQANDYGPQKSSSSKP-----SCSLVAITLG 44
Db 1 MDQQAIAELNLT-----DSGPSSSPSLPRDVCQSPWHQFALKSLCAGILLVL- 53

QY 45 LTTAVLLSVLLYQWILLCOGSNYSTCA-----SCFSCPDRAWKYNHCYFYS 90
Db 54 VVTGLSVSVT-----SLIQKSSIEKCSVDIQQRNKTTERPGLNCPITYWQOLREKCLLFS 109

QY 91 VEEKDWNSSLEFCLARDSHLLVITDQMSLLQVFLSE--AFQWIGLR---NNSGWRWED 145
Db 110 HTVNPWNNSLADCTKESLLLRDDELHHTQNLIRDFKAILFWGLNFSLSKKNWKNIN 169

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QY 146 GSPNFS--RISNSFVOTCGAINKNGLOASSCEVPLHGVCCK 186
Db 170 GSFLNSDLIRGDAKNSCISISQTSVSYEYCSFTEIRWICOK 212

RESULT 7

PCT-US94-07587-2

; Sequence 2, Application PC/TUS9407587

; GENERAL INFORMATION:

; APPLICANT: Schering Corp.

; TITLE OF INVENTION: PURIFIED MAMMALIAN NK ANTIGENS AND

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Schering Corp.

; STREET: One Giralda Farms

; CITY: Madison

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07940

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh 7.1

; SOFTWARE: Microsoft Word 5.1a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/07587

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Lunn, Paul G.

; REGISTRATION NUMBER: 32,743

; REFERENCE/DOCKET NUMBER: DX0397K

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-822-7255

; TELEFAX: 201-822-7039

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 225 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; PCT-US94-07587-2

Query Match 19.6%; Score 201; DB 5; Length 225;

Best Local Similarity 26.0%; Pred. No. 1.1e-13;

Matches 58; Conservative 36; Mismatches 81; Indels 48; Gaps 8;

QY 1 MTDSVIYSMLPTATQAQNDYGPQKSSSSXP-----SCSCLVAITIG 44

Db 1 MDQQAIVAEALNLP-----DSGPSSSPSSLPDRVCGSPWHQFALKSCAGIILLVL- 53

QY 45 LITAVLLSVLLVYQWTLCOGNSYSTCA-----SCPSCPDRMKYGNHCYFVS 90

Db 54 VVTGLSVSVT-----SLIOKSSIEKGSVDITQSSRNKTTTTPGGLNCPYVQQLREKCLLFS 109

QY 91 VEEKDWSLEFLCARDHLVITDNCMSLLQVFLSE--AFCWIGLR---NNSGWRWED 145

Db 110 HTVNPWNNSLADCSKESLLIRDKDELHTQNLRIKAILFWIGLNFSLSEKNKWN 169

QY 146 GSPNFS--RISNSFVOTCGAINKNGLOASSCEVPLHGVCCK 186

Db 170 GSFLNSDLIRGDAKNSCISISQTSVSYEYCSFTEIRWICOK 212

RESULT 8

US-08-690-095-9

; Sequence 9, Application US/08690095

; Patent No. 5792648

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/690,095

; FILING DATE: Filed Herewith

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0110 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 179 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 1098617

; US-08-690-095-9

Query Match

Best Local Similarity 32.7%; Pred. No. 2.4e-13;

Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSQLVAITIGLITAVLLSVLLVYQWTLCOGNS--YSTCASCPCSPDRMKYGNHCYFVSVE 92

Db 20 CILSMA-TLGIILKNSFTKLSIEPAFTPGPNIELQKSDCCQCKWVGYRCNCYFISSE 78

QY 93 EKWNSSLEFLCARDHLVITDNCMSLLQVFLSEAFCEWIGL---RNSGWRWEDGSPL 149

Db 79 QRTWNSRHLCASQSSSLQLQNTDELDFMS--SSQFYWIGLSYSEEHIAWLGSGAL 136

QY 150 NPSRISSNSF----VQTGAINKNG-LOASSCEVPLHGVCCK 186

Db 137 --SQVLFPSFETFTNKCIAYNPNGNALDESCEDKNRYICKQ 176

RESULT 9

US-08-650-578-2

; Sequence 2, Application US/08650578

; Patent No. 5811284

; GENERAL INFORMATION:

; APPLICANT: Chang, Chiwen

; APPLICANT: Aramburu Beltran, Jose

; APPLICANT: Lopez-Botet, Miguel

; APPLICANT: Phillips Jr., Joseph H.

; APPLICANT: Lanier, Lewis L.

; TITLE OF INVENTION: Purified Mammalian NK Antigens and

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute

; STREET: 901 California Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

```
;
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650,578
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,339
; FILING DATE: 29-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-650-578-2

Query Match 19.2%; Score 196.5; DB 2; Length 179;
Best Local Similarity 32.7%; Pred. No. 2.4e-13;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCIVAITGLLPAVLLSVLLYQWILCQGSN--YSTCASCPCSPDRMKYGNHCYFVSVE 92
Db 20 CLSIMA-TLGILLKNSFTKLSIEPAFTPGNIELQKSDCCSQEKWVGRCNCYFISSE 78
QY 93 EKDNSSLEFCLARDSHLLVITDQMSLLQVFLSEAFWCWGL---RNNSGRWEDGSP 149
Db 79 OKTWNSRHLCASQKSLQLQNTDELDFMS--SSQQFYWIGLSYEHTAWLWENGSA 136
QY 150 NFRISNSF----VOTCGAINKNG-LQASSCEVPLHGVCCK 186
Db 137 --SQYLFPSPTETNTKNCIAYNFGNALDESCEDKKNRYICKQ 176

RESULT 10
US-08-688-342-3
; Sequence 3, Application US/08/688342
; Patent No. 5871964
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/688,342
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/688,342
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids

;
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650,578
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,339
; FILING DATE: 29-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-650-578-2

Query Match 19.2%; Score 196.5; DB 2; Length 179;
Best Local Similarity 32.7%; Pred. No. 2.4e-13;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCIVAITGLLPAVLLSVLLYQWILCQGSN--YSTCASCPCSPDRMKYGNHCYFVSVE 92
Db 20 CLSIMA-TLGILLKNSFTKLSIEPAFTPGNIELQKSDCCSQEKWVGRCNCYFISSE 78
QY 93 EKDNSSLEFCLARDSHLLVITDQMSLLQVFLSEAFWCWGL---RNNSGRWEDGSP 149
Db 79 OKTWNSRHLCASQKSLQLQNTDELDFMS--SSQQFYWIGLSYEHTAWLWENGSA 136
QY 150 NFRISNSF----VOTCGAINKNG-LQASSCEVPLHGVCCK 186
Db 137 --SQYLFPSPTETNTKNCIAYNFGNALDESCEDKKNRYICKQ 176

RESULT 11
US-09-113-788-3
; Sequence 3, Application US/09113788
; Patent No. 5969104
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,788
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/688,342
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098616
US-09-113-788-3

Query Match 19.2%; Score 196.5; DB 2; Length 179;
Best Local Similarity 32.7%; Pred. No. 2.4e-13;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;
QY 35 CSCVAITLGLTAVLLSVLLYQWILCOGSN--YSTCASCPCSPDRWMKYGNHCYFVSVE 92
Db 20 CLSLMA-TLGLLKNSTFKLSIEPAFTPGPIELQKSDCCSCQEKWGYRCNCYFISSE 78
QY 93 EKDNSSLEFCLARDSHLLVITDQEMSLLOVFISEAFMWGL---RNNSGWRWEDGSPL 149
Db 79 QKTWNEHRLCASQKSSLLQNTDQLDFMS--SSQQFYWIGLSYSEHTAWLWENGSA 136
QY 150 NFSRISSNSP----VOTCGAINKNG-LOASCEVPLHGVCKK 186
Db 137 --SQYLPSPFTFTKNCIAYNPNGNALDESCEDKKNRYICKQ 176

RESULT 12

US-09-113-789-9
; Sequence 9, Application US/09113789
; Patent No. 6034219
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,789
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/690,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0110 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098617
US-09-113-789-9

Query Match 19.2%; Score 196.5; DB 3; Length 179;
Best Local Similarity 32.7%; Pred. No. 2.4e-13;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;
QY 35 CSCVAITLGLTAVLLSVLLYQWILCOGSN--YSTCASCPCSPDRWMKYGNHCYFVSVE 92
Db 20 CLSLMA-TLGLLKNSTFKLSIEPAFTPGPIELQKSDCCSCQEKWGYRCNCYFISSE 78
QY 93 EKDNSSLEFCLARDSHLLVITDQEMSLLOVFISEAFMWGL---RNNSGWRWEDGSPL 149
Db 79 QKTWNEHRLCASQKSSLLQNTDQLDFMS--SSQQFYWIGLSYSEHTAWLWENGSA 136
QY 150 NFSRISSNSP----VOTCGAINKNG-LOASCEVPLHGVCKK 186
Db 137 --SQYLPSPFTFTKNCIAYNPNGNALDESCEDKKNRYICKQ 176

RESULT 13

PCT-US93-10418-4
; Sequence 4, Application PC/TUS9310418
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Steven F.
; APPLICANT: Hjerrild, Kathryn A.
; TITLE OF INVENTION: Activation Antigen CD69
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10418
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2610-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-10418-4

Query Match 19.2%; Score 196.5; DB 5; Length 199;
Best Local Similarity 27.2%; Pred. No. 2.7e-13;
Matches 52; Conservative 27; Mismatches 79; Indels 33; Gaps 7;
QY 17 QAQNDYGPQ---QKSSSKPSCSLVAITLGLLTAVLLSVLLYQWILCOGSNYSTCASC 73
Db 18 RGQKDHGTSHPEKHHEG---SIQVSIPIWAVLIVLITSLITIALNLNVGKY----NCP 69
QY 74 -----SCPDWKMKGNYHCYFVSVEKDNSSLEFCLARDSHLLVITDQEM 119
Db 70 GLYEKLESSDHVATCKNEWISYKRTCYFFSTTKSWALAQSSCEDARTLAVIDSEKDM 129
QY 120 SILQVFISEAFMWGLRN--NSGWRWEDGSPLN--FSRISNSFVQTGAINKNGLOASS 175
Db 130 TFLKRYSGELEHWIGLKNQANQTKWANGKFNFWNLGTSG----RCVSVNHKNVTAYD 185
QY 176 CEVPLHGVCKK 186

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Db      186 CEANFWVCSK 196

RESULT 14
US-09-055-095-4
; Sequence 4, Application US/09055095
; Patent No. 5945308
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Patterson, Chandra
; APPLICANT: Corley, Neil C.
; APPLICANT: Sather, Susan
; TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/055,095
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0500 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1902982
; US-09-055-095-4

Query Match      18.9%; Score 193; DB 2; Length 270;
Best Local Similarity 30.6%; Pred. No. 9.8e-13;
Matches 44; Conservative 25; Mismatches 53; Indels 22; Gaps 5;

QY      57 QWILCOGSNYSTCASCPCDRMKYGNHCYFVSVEKDWNSLSLEFCCLARDSHLLVITDN 116
Db      127 QEVLEKAANY-----GPCPDWLWHEENCYQFSSGSGFNWKSQENCLSLDAHLKINST 181

QY      117 QEMSLQVFLSEAF--CWIGL---RNSGWRWEDGSPLN-----FSRISNSFVQT 162
Db      182 DELEFIQOMIAHSSFFPFWGLSMRKPNYSWLWEDGTPLTFLPRIQGAVERMYPSG---T 238

QY      163 CGAINKNGLOASSCEVPLHGVCVK 186
Db      239 CAYIQGTVEAENCILTAFSICQK 262

Search completed: August 10, 2004, 16:20:31
Job time : 15.7186 secs

RESULT 15
US-08-809-494A-2
; Sequence 2, Application US/08809494A
; Patent No. 5962260
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; GENERAL INFORMATION:
; APPLICANT: Sawamura, Tatsuya
; APPLICANT: Masaki, Tomoo
; TITLE OF INVENTION: Modified Low-Density Lipoprotein
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAulay Fisher Nissen Goldberg & Kiel
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,494A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-321705
; FILING DATE: 30-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-214206
; FILING DATE: 31-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E
; REGISTRATION NUMBER: 24408
; REFERENCE/DOCKET NUMBER: JG-YY-4363PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 986-4090
; TELEFAX: 212 818-9479
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-494A-2

Query Match      18.9%; Score 193; DB 2; Length 270;
Best Local Similarity 30.6%; Pred. No. 9.8e-13;
Matches 44; Conservative 25; Mismatches 53; Indels 22; Gaps 5;

QY      57 QWILCOGSNYSTCASCPCDRMKYGNHCYFVSVEKDWNSLSLEFCCLARDSHLLVITDN 116
Db      127 QEVLEKAANY-----GPCPDWLWHEENCYQFSSGSGFNWKSQENCLSLDAHLKINST 181

QY      117 QEMSLQVFLSEAF--CWIGL---RNSGWRWEDGSPLN-----FSRISNSFVQT 162
Db      182 DELEFIQOMIAHSSFFPFWGLSMRKPNYSWLWEDGTPLTFLPRIQGAVERMYPSG---T 238

QY      163 CGAINKNGLOASSCEVPLHGVCVK 186
Db      239 CAYIQGTVEAENCILTAFSICQK 262

Search completed: August 10, 2004, 16:20:31
Job time : 15.7186 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:12:27 ; Search time 11.9788 Seconds
(without alignments)
1509.673 Million cell updates/sec

Title: US-09-811-367B-3
Perfect score: 1029
Sequence: 1 MADSSYSTLELPEAPQVQD.....GLQASCEVALQWICKKVLV 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	838	81.4	198	2 I59421	mast cell function
2	182	17.7	257	2 I50146	gene 17.5 protein
3	180.5	17.5	227	2 A46467	natural killer cell
4	173.5	16.9	199	2 JH0822	lymphocyte early a
5	164.5	16.0	225	2 J38700	hNKR-P1a protein -
6	163.5	15.9	146	2 JC7135	agkisacutacin beta
7	160.5	15.6	231	2 PT0374	natural killer cell
8	155.5	15.1	156	2 T28141	C type lectin, B 1
9	152.5	14.8	146	2 JC4691	coagulation factor
10	152.5	14.8	1479	2 T42710	mammose receptor,
11	151	14.7	233	2 PT0372	natural killer cell
12	151	14.7	1487	2 S48719	phospholipase-A(2)
13	149	14.5	223	2 E46467	NKR-P1 protein hom
14	149	14.5	404	2 A46274	HIV gp120-binding
15	147.5	14.3	359	2 A43532	aggreitin beta chai
16	146.5	14.2	146	2 JC7105	NK-cell receptor p
17	146.5	14.2	223	2 A35917	NKR-P1 protein hom
18	146	14.2	220	2 C46467	natural killer cell
19	144	14.0	216	2 PT0375	natural killer cell
20	144	14.0	240	2 I54524	asialoglycoprotein
21	144	14.0	301	2 S13165	scavenger receptor
22	143.5	13.9	742	2 JC7595	hepatic lectin 2 -
23	142	13.8	301	1 LNRT2	lectin, galactose/
24	139	13.5	304	2 JX0209	hepatic lectin hom
25	138	13.4	167	1 WNV282	natural killer cell
26	136.5	13.3	170	2 T28140	aggreitin alpha cha
27	135	13.1	144	2 PC7027	asialoglycoprotein
28	133	12.9	311	1 LNHU2A	secretory phosphol
29	132.5	12.9	1326	2 B56395	

30 132.5 12.9 1465 2 A56395 secretory phosphol
31 128 12.4 284 2 S29855 asialoglycoprotein
32 128 12.4 550 2 A28166 Kupffer cell recep
33 127.5 12.4 291 1 LNHI1 hepatic lectin H1
34 127 12.3 207 1 LNCHL hepatic lectin - c
35 126 12.2 284 1 LNRTL hepatic lectin - r
36 123 12.0 2124 2 A28452 proteoglycan core
37 122.5 11.9 1463 2 A53210 phospholipase A2 r
38 122 11.9 1458 1 A49707 phospholipase A2 r
39 122 11.9 2132 1 A55182 aggreacan precursor
40 121.5 11.8 306 2 A42230 lectin M-ASGP-BP p
41 120.5 11.7 262 2 A30573 T-cell surface gly
42 119.5 11.6 260 2 I49049 Ly-49D-GE antigen
43 119 11.6 133 2 A47267 botroceitin alpha c
44 118.5 11.5 323 1 S09702 L-selectin precurs
45 118.5 11.5 385 1 A34015 L-selectin precurs

ALIGNMENTS

RESULT 1

I59421
mast cell function associated antigen - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I59421
R;Guthmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A:Title: A secretion inhibitory signal transduction molecule on mast cells is another C
A:Reference number: I59421; MUID:96016176; PMID:7568140
A:Accession: I59421
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-188 <RES>
A:Cross-references: EMBL:X79812; NID:g1020141; PIDN:CAA56208.1; PID:g1020142
C:Genetics:
A:Gene: mafa

Query Match 81.4%; Score 838; DB 2; Length 188;
Best Local Similarity 80.7%; Pred. No. 1.3e-74;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MADSSYSTLELPEAPQVQDESFKLKVLRPHLSRPAMVALGLLTIVILMSLLMYQRI 60
Db 1 MADSSYSTLELPEAPRVQDSRWKVKAVLRPCVSLVMVALGLLTIVILMSLLLYQRTL 60
Qy 61 CCGSKDSTCSHCPCPILWTRNGSHCYFFGMEKKDWNSSLKFCADKGSLLTTPDNOGVK 120
Db 61 CCGSKGFMCSQCSCPCPNLWNGSHCYFFGMEKRDWNSSLKFCADKGSLLTTPDNOGVN 120
Qy 121 LFGELYGQDPYWTGLRNIDGWRWEGGPAISLRILTNLSIORCGAIHRNGIQASCEVALQ 180
Db 121 LFGELYGVEDFYWTGLRIDGWRWEDGPAISLSILNSVQKCGTIHRCGLHASSCEVALQ 180
Qy 181 WICKKVL 187
Db 181 WICKKVL 187

RESULT 2

I50146
gene 17.5 protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I50146
R;Bernot, A.; Zoorob, R.; Auffray, C.
Immunogenetics 39, 221-229, 1994
A:Title: Linkage of a new member of the lectin supergene family to the chicken Mhc gene:
A:Reference number: I50146; MUID:94164691; PMID:8119728
A:Accession: I50146
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA


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QY 164 AIHRNGLQASSCEVALQWICK 185
Db 175 FLXNTEVSSMECKNLYWICKN 196

RESULT 5
I38700
N;Title: Human NKR-PIA: A disulfide-linked homodimer of the C-type lectin superfamily ex
A;Reference number: I38700; MUID:94358407; PMID:8077657
A;Accession: I38700
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-225 <RES>
A;Cross-references: EMBL:U11276; NID:9538270; PIDN:AAA21605.1; PID:9544496
C;Superfamily: natural killer cell receptor P1; C-type lectin homology
F;94-210/Domain: C-type lectin homology <LCH>

Query Match 16.0%; Score 164.5; DB 2; Length 225;
Best Local Similarity 27.4%; Pred. No. 1.3e-08;
Matches 60; Conservative 32; Mismatches 90; Indels 37; Gaps 10;

QY 1 MDQQAIVAEINLPDTSQSPSSSPUPRDVCQSPWHQFAL---KLSGAGIILLVLVVT 56
Db 1 MDQQAIVAEINLPDTSQSPSSSPUPRDVCQSPWHQFAL---KLSGAGIILLVLVVT 56

QY 46 -LTVILMSLLMYQRILCCG-----SKDSTCSH--CPSPILWTRNGSHCYFSPMEKKDN 97
Db 57 GLSVSVTSLLQKSSIEKSCVDIQOSRNKTTTERPGLLNCPYQQOLREKCLILFSHTVNPWN 116

QY 98 SSLKFCADKGSLLTTPDNQGVKLFGEYLQD---FYWIGLR---NIDGWRWEGGPALS- 150
Db 117 NSLADSTKESLSLLTRDKDEL-IHTQNLIRDKAILEFWIGLNSLSEKNWKNWINGSPLNS 175

QY 151 --LRILNTSLIQRCAIHRNGLQASSCEVALQWICKKVL 187
Db 176 NDLIEIRGDAKENSICISISQTSVYSEYCSTEIRWICQKEL 214

RESULT 6
JC7135
agkisacutacin beta chain precursor - sharp-nosed viper
N;Alternate names: fibrinogenolytic venom protein
C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000
C;Accession: JC7135; PMID:10558903
R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
Biochem. Biophys. Res. Commun. 265, 530-535, 1999
A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenolytic venom
A;Reference number: JC7134; MUID:20025379; PMID:10558903
A;Accession: JC7135
A;Molecule type: protein
A;Residues: 1-146 <CHE>
A;Cross-references: GB:AF176421
A;Experimental source: venom gland
A;Accession: PC7038
A;Molecule type: protein
A;Residues: 24-50;59-83;102-107;112-114 <CH2>
C;Superfamily: tetraneurin; C-type lectin homology
C;Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-146/Product: agkisacutacin beta chain #status experimental <MAT>

Query Match 15.9%; Score 163.5; DB 2; Length 146;
Best Local Similarity 30.2%; Pred. No. 1e-08;
Matches 48; Conservative 15; Mismatches 71; Indels 25; Gaps 6;
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```
QY 35 LSRFAMVALGLLTIVILMSLLMYQRILCCGSKDSTCSHCPSPILWTRNGSHCYFSPMEKK 94
Db 1 MGRFIFVSFGLJLVFL-----SLSGTAADCPs---EWSSEHGCHYKPFDEPK 44

QY 95 DWNSSLKFCAD--KGSLLTTPDNQG---VKLFGEYLQDQFYWIGLRNI-DG--NRWEG 145
Db 45 TWADAEEKFCTQOHKGSGLASFHSSEADFFVILTTLSLKTDLVWIGLKNWNGCYWKWSD 104

QY 146 GPALSILRLTNSLIQRCAIHRNGLQASSCEVALQWICK 184
Db 105 GTKLDYKDWREQECVLVSRTVNNNEWLSMDGTTCSFVCK 143

RESULT 7
PT0374
natural killer cell receptor group 2-C, splice form 1 - human
N;Alternate names: NKG-C
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 19-May-2000
C;Accession: PT0374
R;Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
J. Exp. Med. 173, 1017-1020, 1991
A;Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type I:
A;Reference number: PT0372; MUID:91178434; PMID:2007850
A;Accession: PT0374
A;Molecule type: mRNA
A;Residues: 1-231 <HOU>
A;Cross-references: EMBL:X54869; NID:935060; PIDN:CAA38651.1; PID:935061
A;Experimental source: natural killer cell
C;Genetics:
A;Gene: GDB:KLC2; NKG2-C
A;Cross-references: GDB:9787095
A;Map position: 12p13-12p13
C;Superfamily: natural killer cell receptor P1; C-type lectin homology
C;Keywords: glycoprotein; transmembrane protein
F;71-96/Domain: transmembrane #status predicted <TRA>
F;27,100,149,178/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.6%; Score 160.5; DB 2; Length 231;
Best Local Similarity 24.4%; Pred. No. 3.3e-08;
Matches 41; Conservative 29; Mismatches 83; Indels 15; Gaps 5;

QY 33 PHLRFAMVALGLLTIVILMSLLMYQRIL-----CCGSKDSTCSHCPSPILWTRNG 83
Db 66 PPEKLTAEVLGICIVLWATVLTIVLPFLFQNNSSNPNRTQKARHCHGCHPEEITYS 125

QY 84 SHCYFSPMEKKDWNSSLKFCADKGSLLTTPDNQGVKLFGEYLQDQFYWIGLR-RNIDGWR 142
Db 126 NSCYIGKERTWEESILLACTSKNSLLSIDNEEIKFLASILPSS--WIGVFNSSHP 183

QY 143 WE--GGPALSILRLTNSLIQ-RCGAIHRNGLQASSCEVALQWICKKVL 187
Db 184 WVTINGLAFKHKIKDSDNAELNCALQVNLKSAQCQSSMIYHCKHKL 231

RESULT 8
T28141
C type lectin, B locus - chicken
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T28141
R;Milne, S.; Kaufman, J.; Beck, S.
submitted to the EMBL Data Library, May 1998
A;Description: DNA sequencing and analysis of the chicken major histocompatibility comp.
A;Reference number: Z20475
A;Accession: T28141
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-156 <MIL>
A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292545; PIDN:CAA18961.1
A;Experimental source: clone cB12
C;Genetics:
A;Gene: Blec
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[illegible]

Query Match	14.3%;	Score 147.5;	DB 2;	Length 359;
Best Local Similarity	27.3%;	Pred. No. 9.7e-07;		
Matches 38;	Conservative 19;	Mismatches 61;	Indels 21;	Gaps 6;
Qy	62	CGSKDSTCSHCPCSPILWTNRNGSHCYFYSMEKDDWSSLKFCADKDGSHLLTF----	PDNQ	117
Db	226	CGSAD-TC-----CPSGWIMHOKSCFYISTTSKNWQESQKQCYTLSSKLATFSEIYPQSH	279	
Qy	118	GVKLFGEYL-----QDPEYTWIGLRNIDGRWEGGPPALSIRLITNSLIQRCGAIHRN-----	169	
Db	280	SYFNLNLLPFGGSGNSYWTGLSSNKDWKLTDD---TQRTFTYAQSSKCNKVHKTWSWWT	336	
Qy	170	LQASSCEVALQWICKKVLV	188	
Db	337	LESRCRSLPYICENTAF	355	

Search completed: August 10, 2004, 16:19:36
Job time : 12.9788 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2004, 16:05:41 ; Search time 7.32035 Seconds
(without alignments)
1337.256 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029

Sequence: 1 MADSSIVSTLELPEAPQVQD.....GLQASCEVALQWICKVLY 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	180.5	17.5	179	1	Q9mzK9 macaca mula
2	180.5	17.5	227	1	CD94 MACMU
3	178.5	17.3	179	1	CD94 HUMAN
4	178.5	17.3	179	1	CD94 PANTR
5	173.5	16.9	199	1	CD69 HUMAN
6	168	16.3	199	1	CD69 MOUSE
7	162.5	15.8	233	1	CD94 PANTR
8	158.5	15.4	231	1	CD94 HUMAN
9	158	15.4	233	1	CD94 PANTR
10	152.5	14.8	146	1	CD94 HUMAN
11	151	14.7	233	1	CD94 HUMAN
12	150.5	14.6	148	1	CD94 HUMAN
13	149	14.5	223	1	CD94 HUMAN
14	148	14.4	216	1	CD94 HUMAN
15	147.5	14.3	359	1	CD94 HUMAN
16	146.5	14.2	163	1	CD94 HUMAN
17	146.5	14.2	223	1	CD94 HUMAN
18	146	14.2	220	1	CD94 HUMAN
19	145	14.1	146	1	CD94 HUMAN
20	144	14.0	149	1	CD94 HUMAN
21	144	14.0	216	1	CD94 HUMAN
22	144	14.0	240	1	CD94 HUMAN
23	144	14.0	301	1	CD94 HUMAN
24	139.5	13.6	231	1	CD94 HUMAN
25	139	13.5	157	1	CD94 HUMAN
26	139	13.5	304	1	CD94 HUMAN
27	138	13.4	167	1	CD94 HUMAN
28	138	13.4	240	1	CD94 HUMAN
29	138	13.4	301	1	CD94 HUMAN
30	137.5	13.4	233	1	CD94 HUMAN
31	133.5	13.0	1722	1	CD94 HUMAN
32	133	12.9	311	1	CD94 HUMAN
33	132	12.8	548	1	CD94 HUMAN

34 128 12.4 550 1 KUCR RAT
35 127.5 12.4 290 1 LECH_HUMAN
36 127 12.3 207 1 LECH_CHICK
37 126 12.2 283 1 LECH_MOUSE
38 126 12.2 283 1 LECH_RAT
39 125.5 12.2 133 1 RHCA_AGRH
40 124.5 12.1 117 1 CHBB_CROHO
41 124.5 12.1 123 1 ABAA_TRIAB
42 123 12.0 2134 1 PGCA_RAT
43 122.5 11.9 1463 1 PA2R_BOVIN
44 122 11.9 1458 1 PA2R_RABIT
45 122 11.9 2132 1 PGCA_MOUSE

ALIGNMENTS

RESULT 1
CD94_MACMU STANDARD; PRT; 179 AA.
AC Q9MZK9; Q9GK91; Q9MZK7; Q9MZK8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
DE lectin-like receptor subfamily D, member 1).
GN KURDI OR CD94.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP MEDLINE=20322487; PubMed=10866118;
RA LaBonte M.L., Levy D.B., Letvin N.L.;
RT "Characterization of rhesus monkey CD94/NKG2 family members and
RT identification of novel transmembrane-deleted forms of NKG2-A, B, C,
RT and D.";
RL Immunogenetics 51:496-499 (2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=21158386; PubMed=11261935;
RA Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.;
RT "Selective expression of NKG2-A and NKG2-C mRNAs and novel alternative
RT splicing of 5' exons in rhesus monkey decidua.";
RL Immunogenetics 53:69-73 (2001).
CC -1- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -1- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
CC members.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=CD94-A;
CC IsoId=Q9MZK9-1; Sequence=Displayed;
CC Name=2; Synonyms=CD94-B;
CC IsoId=Q9MZK9-2; Sequence=VSP_003055;
CC Name=3; Synonyms=CD94 alt;
CC IsoId=Q9MZK9-3; Sequence=VSP_003054;
CC TISSUE SPECIFICITY: Natural killer cells.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.

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DR EMBL; AF190931; AAF74527.1; -;
DR EMBL; AF190932; AAF74528.1; -;

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DR EMBL; AF190933; AAF74529.1; -.
DR EMBL; AF294886; AAG34498.1; -.
DR HSP; P22897; IREG.
DR InterPro; IPR001304; Lectin_C.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN_2; 1.
DR PROSITE; PS0041; C-TYPE LECTIN_1; FALSE_NEG.
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing; Polymorphism.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 89 174 BY SIMILARITY.
FT DISULFID 152 166 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 1 34 MAVPKTTLWRLISGLTGLICLSLWATLGLKNS -> MAA
(in isoform 3).
FT FTID=VSP_003054.
FT L-> LQ (in isoform 2).
FT FTID=VSP_003055.
FT Y -> D.
FT VARIANT 139 139 06212B4494527F07 CRC64;
SQ SEQUENCE 179 AA; 20607 MW; 06212B4494527F07 CRC64;
Query Match 17.5%; Score 180.5; DB 1; Length 179;
Best Local Similarity 31.8%; Pred. NO. 6e-11;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;
QY 44 GLLTVLMSLLMYQRILCGS-----KSTCHPCSPILLWTRNGS 84
DB 14 GTLGLICSLWATLGLICLSLWATLGLKNSDSC--C-SCHKWVGVC 70
QY 85 HCYFSEMEKQDWNLSKFCADKSHLLTFPDNGQVKLFGEYLGQDFYWGRLNID---GW 141
DB 71 NCYFISSEKTNWNSRHFCASQKSLQLQNRDELDFNS--SQHFYIGLSYSEHTAW 128
QY 142 RWEQGPALSLILNLSLI---QRCGAIHRNG-LQASSCEVALQWICKVLY 187
DB 129 LWENGSAISQYLFPSFTFKPKNCIAYNSKGNALDESCETKNRYICKQOL 178

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RESULT 2

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NKIL MOUSE STANDARD; PRT; 227 AA.
AC P27811;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Natural killer cell surface protein Fl-2 (NKR-P1 2) (NKR-P1.7).
GN KIRBIA OR LY55A OR LY55.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91349596; PubMed=1880421;
RA Giorda R., Trucco M.,
RT "Mouse NKR-P1. A family of genes selectively coexpressed in adherent
RL lymphokine-activated killer cells.";
RL J. Immunol. 147:1701-1708(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92013158; PubMed=1680927;
RA Yokoyama W.M., Ryan J.C., Hunter J.J., Smith H.R.C., Stark M.,
RA Seaman W.E.;
RT "cDNA cloning of mouse NKR-P1 and genetic linkage with LY-49.
RT Identification of a natural killer cell gene complex on mouse
RT chromosome 6.";

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J. Immunol. 147:3229-3236(1991).
-!- FUNCTION: May function as signal-transmitting receptor.
-!- SUBUNIT: Homodimer; disulfide-linked.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- TISSUE SPECIFICITY: Natural killer cells.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
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CC -----
CC EMBL; M77676; AAA39822.1; -.
CC EMBL; M77753; AAA39366.1; -.
CC PIR; A46467; A46467.
CC HSP; P22897; IREG.
CC MGD; MGI:107540; K1rb1a.
CC InterPro; IPR002353; AntifreezeII.
CC InterPro; IPR001304; Lectin_C.
CC Pfam; PF00059; lectin_c; 1.
CC PRINTS; PR00356; ANTIFREEZEII.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG.
CC PROSITE; PS0041; C-TYPE LECTIN_2; 1.
KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 43 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 63 227 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 93 212 C-TYPE LECTIN (LONG FORM).
FT DISULFID 94 105 BY SIMILARITY.
FT DISULFID 122 210 BY SIMILARITY.
FT DISULFID 189 202 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 39 39 S -> L (IN REF. 2).
SQ SEQUENCE 227 AA; 25689 MW; 0599A2587DF08615 CRC64;
Query Match 17.5%; Score 180.5; DB 1; Length 227;
Best Local Similarity 26.7%; Pred. NO. 7.8e-11;
Matches 58; Conservative 33; Mismatches 95; Indels 31; Gaps 8;
QY 1 MADSIYSTLELPEAPQVQDESRLK---KAVLHRPHLSRFAMVALGLL---TVILMSL 53
DB 1 MDTARVYFGLKPPRTPGAWHESPSPDPACRPSRHSALKSCAGLILLVVTLLGMSV 60
QY 54 LMVORILC-----CG-----SKDSTCHPCSPILWTRNGSHCYFSEMEKQDWNSS 99
DB 61 LV--RVLLQKPSIEKCYVLIQENLNKNTDCAKLECPQDWLSHRDKCFHVQSVNTWEEG 118
QY 100 LKFCADKSGHLLTFPDNGQVKLFGEYLGQDF--YWGRLNII---DGNWEGGPALSL--L 151
DB 119 LVDGCDGKATLMLIQDQELRFLDLSIKEKYNSEFWIGLYTLPDMNWKWINGSTLNSDVL 178
QY 152 RILNLSLQRCGAIHRNGLOASSCEVALQWICKVLY 188
DB 179 KITGDTENDSCAAISGDKVTFESCNSDNRRWICKQELY 215

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RESULT 3

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CD94_HUMAN
ID CD94_HUMAN STANDARD; PRT; 179 AA.
AC Q13241; O43321; O43773; Q9UBE3; Q9UEQ0;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
DE lectin-like receptor subfamily D, member 1) (KF43).
GN KIR2D1 OR CD94.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC MEDLINE=96011848; PubMed=7589107;
RX Chang C., Rodriguez A., Carretero M., Lopez-Botet M., Phillips J.H.,
RA Ianier L.L.;
RT "Molecular characterization of human CD94: a type II membrane
RT glycoprotein related to the C-type lectin superfamily.";
RL Eur. J. Immunol. 25:2433-2437(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96139529; PubMed=9472066;
RA Rodriguez A., Carretero M., Glienke J., Bellon T., Ramirez A.,
RA Leirach H., Francis F., Lopez-Botet M.;
RT "Structure of the human CD94 C-type lectin gene.";
RL Immunogenetics 47:305-309(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Blassoni R.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=96267245; PubMed=9601951;
RA Furukawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T., Tadokoro K.,
RA Tohma S., Inoue T., Yamamoto K., Juji T.;
RT "A alternatively spliced form of the human CD94 gene.";
RL Immunogenetics 48:87-88(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S., Loughlano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
CC members.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=CD94-A;
CC IsoId=Q13241-1; Sequence=Displayed;
CC Name=2; Synonyms=CD94-B;
CC IsoId=Q13241-2; Sequence=VSP_003053;
CC Name=3; Synonyms=CD94 alt;
CC IsoId=Q13241-3; Sequence=VSP_003052;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD94 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd94.htm".

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CC -----
DR EMBL; U30610; AAC50291.1; -
DR EMBL; Y14287; CAA74663.1; -
DR EMBL; Y14288; CAA74663.1; JOINED.
DR EMBL; AJ000673; CAA04230.1; -
DR EMBL; AJ000001; CAA03845.1; -
DR EMBL; AB009597; BAA24450.1; -
DR EMBL; AB010084; BAA24451.1; -
DR EMBL; BC028009; AAH28009.1; -
DR PDB; 1B6E; 15-JUN-99.
DR Genew; HGNC:6378; KLRD1.
DR MIM; 602894; -
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . ; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . ; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SMO0034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing; 3D-structure.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT
FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 89 174 BY SIMILARITY.
FT DISULFID 152 166 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 34 MAVEKTLMLRLISGTGLICLSLMTATGILLKNS -> MAA
FT (in isoform 3)
FT /FTID=VSP_003052.
FT VARSPLIC 105 105 L -> LQ (in isoform 2).
FT /FTID=VSP_003053.
SQ SEQUENCE 179 AA; 20497 MW; 1884D99E8D9583A7 CRC64;
Query Match 17.3%; Score 178.5; DB 1; Length 179;
Best Local Similarity 31.8%; Pred. No. 9.5e-11;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;
QY 44 GLITVILMSLLMYQRIILCCGS-----KSTCSHCPCSPILWTRNGS 84
DB 14 GTLGIICLSLMTATGILLKNSFTKLSIEPAFTGPNIELQKSDC--C-SCQEKWGYRC 70
QY 85 HCYYFNEKKDWNSSLKFCADKSHLLTTPDNGVKLFGYLGQDFYGLRND---GW 141
DB 71 NCYFISSEKQTNWESRHLKASQSKSLQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128
QY 142 RWEGGALSRLITN---SLIQCGAIHRNG-LQASCEVALQWICKYVL 187
DB 129 LWENGALSQYLPFPSTFTNTKNCIAYPNNGNALDESCDKNYICKQQL 178
RESULT 4
CD94_PANTR
ID CD94_PANTR STANDARD; PRT; 179 AA.
AC Q9MZ41;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell

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DR InterPro; IPR002353; AntifreezeZell.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTIFREEZE1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
DR Antigen; Signal-anchor; Transmembrane; Lectin; Glycoprotein;
KW Phosphorylation.
KW DOMAIN 1 40 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 41 61 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 62 199 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 92 195 C-TYPE LECTIN.
FT DISULFID 68 85 BY SIMILARITY.
FT DISULFID 96 194 BY SIMILARITY.
FT DISULFID 173 186 BY SIMILARITY.
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 199 AA; 22517 MW; 39F8E4941D36D4F6 CRC64;

Query Match 16.3%; Score 168; DB 1; Length 199;
Best Local Similarity 24.1%; Pred. No. 1.2e-09;
Matches 39; Conservative 34; Mismatches 67; Indels 22; Gaps 5;

QY 38 FAWALGLLTIVILMSLL-----MYQRIILCCGSKDSTCSHCPCPILWTRNGSHC 86
Db 43 WAVILVILTSLLIALALNKGKYNCPGLYEKL-----ESSDHHVATCKNEWISYKRTC 96
QY 87 YFFSTTYKSWALQSCSDAATLAVIDSEKDMFLKRYSELEHNLGKNEAQTWKWA 144
Db 97 YFFSTTYKSWALQSCSDAATLAVIDSEKDMFLKRYSELEHNLGKNEAQTWKWA 156

QY 145 GGPAL-SURLTNSLIQRCGAHNRGLQASCEVALQWICKK 185
Db 157 NGKEFNWFNLTGSG--GRCSVNHNKNTAVDCEANFHWVCSK 196

RESULT 7
NKGC PANTR STANDARD; PRT; 233 AA.
AC Q9GME8; Q9MZ38; Q9MZ40;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE NKG2-C type II integral membrane protein (NGK2-C activating NK
DE receptor) (NK cell receptor C).
GN KLR2C OR NKG2C.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS ASP-60 AND 232-TYR-ARG-233 DEL.
RX MEDLINE=20350666; PubMed=10894168;
RA Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,
RA Muir D.G., Canavez F., Cooper S.L., Vallante N.M., Lanier L.L.,
RA Farham P.;
RT "Rapid evolution of NK cell receptor systems demonstrated by
RT comparison of chimpanzees and humans.";
RL Immunity 12:687-698(2000).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC Class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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DR EMBL; AF259057; AAF86967.1; -.
DR EMBL; AF259059; AAF86969.1; -.
DR EMBL; AF259060; AAF86970.2; -.
DR HSP; P05451; LLIT.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein.
KW DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 93 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 94 233 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 116 229 C-TYPE LECTIN (LONG FORM).
FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 145 227 BY SIMILARITY.
FT DISULFID 206 219 BY SIMILARITY.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 60 60 N -> D (in allele NKG2-C*101).
FT VARIANT 232 233 Missing (in allele NKG2-C*103).
SQ SEQUENCE 233 AA; 26169 MW; 18C04D1B91E1B7CA CRC64;

Query Match 15.8%; Score 162.5; DB 1; Length 233;
Best Local Similarity 25.4%; Pred. No. 5.1e-09;
Matches 43; Conservative 28; Mismatches 83; Indels 15; Gaps 5;

QY 33 PHLRFAMVALGLLTIVILMSLLMYQRIILCCGSKDSTCS-----HCPCPILWTRNG 83
Db 66 PPPEKLFAVLGIICVVMATVLTIVILPELQNNSSPNTGTOKARHCPCPEWITYS 125
QY 84 SHCYFMEKKDMNSSLKFCADKSHLLTDPDNGVKLFGYLGQDFYIGL-RNIDGWR 142
Db 126 NSCYIIGKERTWEESLLACTSKNSGLSIDNBEEMKFLATISPS--WIGVFNSSHP 183
QY 143 WE--GGPALSURLTNSLIQ--RCGAHNRGLQASCEVALQWICKKVLV 188
Db 184 WVTINGLAFKHEIIDSDAELNCAVLQVGLKLSAQCGSSIIYHCKHKLY 232

RESULT 8
NKGC HUMAN STANDARD; PRT; 231 AA.
AC P26717; O43802; Q9NR42;
DT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NKG2-C type II integral membrane protein (NGK2-C activating NK
DE receptor) (NK cell receptor C).
GN KLR2C OR NKG2C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91178434; PubMed=2007850;
RA Houchins J.P., Yabe T., McSherry C., Bach F.H.;
RT "DNA sequence analysis of NKG2, a family of related cDNA clones
RT encoding type II integral membrane proteins on human natural killer
RT cells.";
RN J. Exp. Med. 173:1017-1020(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98350122; PubMed=9683661;
RA Glienke J., Sobanov Y., Brostjan C., Steffens C., Nguyen C.,
RA Lehrach H., Hofer E., Francis F.;
RT "The genomic organization of NKG2C, E, F, and D receptor genes in the

```

human natural killer gene complex.";

[3]

SEQUENCE FROM N.A.

RA Biassoni R.;

RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

[4]

SEQUENCE FROM N.A., AND VARIANTS ASN-2 AND PHE-102.

EX MEDLINE=21623889; PubMed=11751968;

RA Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,

RA Cleland S., Guethlein L.A., Uhrberg M., Parham P.;

RT "Conservation and variation in human and common chimpanzee CD94 and

RT NKG2 genes.";

RN J. Immunol. 168:240-252(2002).

CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC

CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.

CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.

CC -!- SUBCELLULAR LOCATION: Type II membrane protein.

CC -!- TISSUE SPECIFICITY: Natural killer cells.

CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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EMBL; X54869; CAA38651.1; --

EMBL; AJ001684; CAA04922.1; --

EMBL; Y13055; CAA73498.1; --

EMBL; AF260134; AAF86972.1; --

PIR; PT0374; PT0374.

DR Genew; HGNC:6375; KIRC2.

DR MIM; 602891; --

DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0004888; F:transmembrane receptor activity; TAS.

DR GO; GO:0006968; P:cellular defense response; TAS.

DR GO; GO:0007165; P:signal transduction; TAS.

DR InterPro; IPR001304; Lectin_C.

DR Pfam; PF00059; Lectin_c; 1.

DR SMART; SM00034; CLECT_1.

DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.

DR PROSITE; PSS00041; C_TYPE_LECTIN_2; 1.

KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;

KW Glycoprotein; Polymorphism.

FT DOMAIN 1 70

FT TRANSMEM 71 93

FT CYTOPLASMIC (POTENTIAL).

FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

FT (POTENTIAL).

FT EXTRACELLULAR (POTENTIAL).

FT C-TYPE LECTIN (LONG FORM).

FT BY SIMILARITY.

FT BY SIMILARITY.

FT BY SIMILARITY.

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT S -> N (in allele NKG2-C*02).

FT /FTid=VAR_013404.

FT S -> F (in allele NKG2-C*02).

FT /FTid=VAR_013405.

FT M -> I (IN REF. 1).

FT CONFLICT 161 161

FT SEQUENCE 231 AA; 26072 MW; 6B971EECD7542930 CRC64;

Query Match 15.4%; Score 158.5; DB 1; Length 231;

Best Local Similarity 24.4%; Pred. No. 1.3e-08;

Matches 41; Conservative 29; Mismatches 83; Indels 15; Gaps 5;

QY 33 PHLSRFAMVAGLLTVILMLLYQRL-----CCGSKDSTCHSCPCFLWPRNG 83

DB 66 PPPEKLTAEVLGIICVLMATVLKTVILPFLQNSSPNRTQKARHCGHCEEMITYS 125

QY 84 SHCYFMSNEKKDNSSLKPCADKSGSHLLTPDNGVKLFGELYQDFYWGIL-RNIDGWR 142

DB NSCYIIGKERRTWEEISLLACTSKNSLLSIDNEEMKFLASILPSS--WIGVFNSSHP 183

QY 143 WE--GGPALSRILRLTSLIQ--RCGAIHNRGLQASSCEVALQWICKKVL 187

DB WVTIINGLAFKHKIKDSNAELNCAVLQVNRKSAQCGSSMIYHCKHKL 231

RESULT 9

KG PANTR STANDARD; PRT; 233 AA.

AC Q95MI5; Q9MTM6;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE NKG2-A/NKG2-B type II integral membrane protein (NKG2-A/B activating

DE NK receptor) (NK cell receptor A).

GN KIRC1 OR NKG2A.

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

OX NCBI_TaxID=9598;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20350666; PubMed=10894168;

RA Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,

RA Muir D.G., Canavez F., Cooper S.L., Valiante N.M., Lanier L.L.,

RA Parham P.;

RT "Rapid evolution of NK cell receptor systems demonstrated by

RT comparison of chimpanzees and humans.";

RL Immunity 12:687-698(2000).

RN [2]

RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND VARIANTS LEU-79 AND

RP ARG-231.

RX MEDLINE=21623889; PubMed=11751968;

RA Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,

RA Cleland S., Guethlein L.A., Uhrberg M., Parham P.;

RT "Conservation and variation in human and common chimpanzee CD94 and

RT NKG2 genes.";

RL J. Immunol. 168:240-252(2002).

CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC

CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.

CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.

CC -!- SUBCELLULAR LOCATION: Type II membrane protein.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=NKG2-A;

CC IsoId=Q95MI5-1; Sequence=Displayed;

CC Name=NKG2-B;

CC IsoId=Q95MI5-2; Sequence=VSP_003066;

CC -!- TISSUE SPECIFICITY: Natural killer cells.

CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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EMBL; AF259055; AAF86965.1; --

EMBL; AF259056; AAF86966.1; --

EMBL; AF350005; AAK83792.1; --

InterPro; IPR001304; Lectin_C.

PIR; PF00059; Lectin_c; 1.

DR SMART; SM00034; CLECT_1.

DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.

DR PROSITE; PSS00041; C_TYPE_LECTIN_2; 1.

KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;

KW Glycoprotein; Alternative splicing; Polymorphism.

```
FT DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 93 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 94 233 C-TYPE LECTIN (LONG FORM).
FT DOMAIN 118 231 BY SIMILARITY.
FT DISULFID 119 130 BY SIMILARITY.
FT DISULFID 147 229 BY SIMILARITY.
FT DISULFID 208 221 BY SIMILARITY.
FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 96 113 Missing (in isoform NKG2-B).
FT VARIANT 79 79 I -> L (in NKG2-A*03).
FT VARIANT 231 231 H -> R (in NKG2-A*03).
SQ SEQUENCE 233 AA; 26212 MW; AE9BBA3A0209984 CRC64;

Query Match 15.4%; Score 158; DB 1; Length 233;
Best Local Similarity 23.5%; Pred. No. 1.4e-08;
Matches 46; Conservative 29; Mismatches 85; Indels 36; Gaps 6;

QY 7 YSTLELPAPQVQDSRWKLVKAVLRPHLSRFAMVALGLTFLM-----SLIM 55
DB 59 YHCKDLPSAPE-----KLIIVGILGHICLILMASVVTIIVIPSTLIQ 99
QY 56 YQRIILCCGSKDSTCSHCPSPILWTRNGSHCVYFMEKKDWNNSLKFCAKDGSHLLTPPD 115
DB 100 RHNNSSLNTRQKARHCCHCEPEWITYNSCVYIGKERTWEESLLACTSKNSGLISDN 159
QY 116 NQGVKLFGEYLQDQFYWIGL-RNIDGWEWE--GGPALSRLILNLSLIQ-RCGAIHRNGLQ 171
DB 160 EEMKFLS--IISPSWIGVFRNSHHPWVTINGLAFKHEIKSDNAELNCAVLQVNGLK 217
QY 172 ASSCEVALQWICKVL 187
DB 218 SAQCGSSIIYHCKHKL 233

RESULT 10
IXB_TRIFL
ID IXB_TRIFL STANDARD; PRT; 146 AA.
AC P23807; Q91247;
DT 01-NOV-1991 (Rel. 20, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Coagulation factor IX/factor X-binding protein B chain precursor (IX/X-BP).
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=88087;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96184662; PubMed=86453114;
RA Matsuzaki R., Yoshihara E., Yamada M., Shima K., Atoda H., Morita T.;
RT "cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from snake venom."
RT Biochem. Biophys. Res. Commun. 220:382-387(1996).
RL [2]
RN SEQUENCE OF 24-146.
RP TISSUE=Venom;
RX MEDLINE=91332000; PubMed=18311197;
RA Atoda H., Hyuga M., Morita T.;
RT "The primary structure of coagulation factor IX/factor X-binding protein isolated from the venom of Trimeresurus flavoviridis. Homology with asialoglycoprotein receptors, proteoglycan core protein, tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E."
RT J. Biol. Chem. 266:14903-14911(1991).
RL [3]
RN [3]
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RP MEDLINE=97331317; PubMed=9187649;
```

```
RA Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;
RT "Structure of coagulation factors IX/X-binding protein, a heterodimer of C-type lectin domains."
RL Nat. Struct. Biol. 4:438-441(1997).
CC -!- FUNCTION: Anticoagulant protein which binds with factor IX and factor X in the presence of calcium with a 1 to 1 stoichiometry.
CC -!- SUBUNIT: Heterodimer of chains A and B; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: Calcium is required for ligand binding.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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CC
CC -----
CC EMBL; D83332; BAAL1888.1; -.
CC PIR; JC4691; JC4691.
CC PDB; 1LXX; 06-MAY-98.
CC PDB; 1BJ3; 16-AUG-99.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR003990; Pancreatins_ac.
CC Pfam; PF00059; Lectin_C; 1.
CC PRINTS; PR01504; PNCREATITSAP.
CC SMART; SM00034; CLECT; 1. LECTIN_1; 1.
CC PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
CC PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
CC Lectin; Calcium; Signal; 3D-structure.
FT SIGNAL 1 23
FT CHAIN 24 146
FT COAGULATION FACTOR IX/FACTOR X-BINDING
FT PROTEIN B CHAIN.
FT C-TYPE LECTIN (LONG FORM).
FT BY SIMILARITY.
FT BY SIMILARITY.
FT INTERCHAIN (WITH C-102 IN A CHAIN).
FT BY SIMILARITY.

Query Match 14.8%; Score 152.5; DB 1; Length 146;
Best Local Similarity 24.5%; Pred. No. 3.1e-08;
Matches 39; Conservative 25; Mismatches 70; Indels 25; Gaps 5;

QY 35 LSRFAMVALGLTFLMISLLMYQRIILCCGSKDSTCSHCPSPILWTRNGSHCVYFMEKK 94
DB 1 MGRFIFMGFGLWFL-----SLSGTAADCPD---WSSVEGHCHYKPSSEPK 44
QY 95 DWNSSLKFCADK--GSHLLTTPDNOG---VKLFGVYLQDQFYWIGLRLNI---DQWRWEG 145
DB 45 NWADAEENCTQOHAGCHLVSVFQSSSEADFFVKLAFQTFGHSIFFWGLSNVWQCNQWSEN 104
QY 146 GPALSRLILNLSLIQRCGAIHRNGLQASCEVALQWICK 184
```


47 TWADAEXFCTQOHTGSHLVSPHSTEEVDVFFVVMTHQSLKSTFFWIGANNIWNKCNQWQSD 106

Db 172 ASSCEVALQWICKKVL 187
QY 146 G 146
Db 107 G 107

RESULT 12

CVXB_CRODU
ID CVXB_CRODU STANDARD; PRT; 148 AA.
AC 093427;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Convulxin beta precursor (CVX beta).
OS Convulxin durissus terrificus (South American rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Viperidae; Crotalinae; Crotalus.
OC NCBI_TaxID=8732;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-53; 99-109 AND 126-145.
RC TISSUE=Venom gland;
RX MEDLINE=98324901; PubMed=9657980;
RA Leduc M., Bon C.;
RT "Cloning of subunits of convulxin, a collagen-like platelet-
RT aggregating protein from Crotalus durissus terrificus venomom.";
RL Biochem. J. 333:389-393(1998).
CC -!- FUNCTION: Binds to the platelet and collagen receptor,
CC glycoprotein VI (GPVI).
CC -!- SUBUNIT: Heterohexamer of three alpha chains and three beta
CC chains; disulfide-linked.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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CC
CC EMBL; Y16349; CAA76182.1; -.
DR HSP; P23807; IIXX.
DR InterPro; IPR001304; Lectin C.
DR InterPro; IPR003990; Pancreatis_ac.
DR Pfam; PF00059; lectin c; 1.
DR PRINTS; PR01504; PNCREATITSP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
KW Lectin; Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 148
FT DOMAIN 34 145
FT DISULFID 26 26
FT INTERCHAIN (WITH C-158 IN ALPHA CHAIN)
FT (POTENTIAL).
FT BY SIMILARITY.
FT DISULFID 27 38
FT DISULFID 55 144
FT DISULFID 100 100
FT INTERCHAIN (WITH C-104 IN ALPHA CHAIN)
FT (POTENTIAL).
FT BY SIMILARITY.
FT DISULFID 121 136
FT SEQUENCE 148 AA; 17402 MW; 94D7E3E1BC693B9F CRC64;
Query Match
Best Local Similarity 14.6%; Score 150.5; DB 1; Length 148;
Matches 38; Conservative 18; Mismatches 42; Indels 23; Gaps 6;
QY 35 LSRFAMVAGLTLVILMSLLMYQRLCCGSKDSTCHSPCLILWTRNGSHCYFYSMEKK 94
Db 1 MGRFIFVSPGLL-VVPLSL-----SGSEAGFC-----CPSHWSYDRYCYKVFQDM 46
QY 95 DWNSSLKFCADK-GSHLTFFPDNQ-----VKLFGYLQDFYWLGLRNI---DGMWEG 145

RESULT 13

NK12_MOUSE
ID NK12_MOUSE STANDARD; PRT; 223 AA.
AC P27812;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Natural killer cell surface protein P1-34 (NKR-P1 34).
GN KLRB1B OR LY55B OR LY55-B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91349596; PubMed=1880421;
RA Giordano R., Trucco M.;
RT "Mouse NKR-P1. A family of genes selectively coexpressed in adherent
RT lymphokine-activated killer cells.";
RL J. Immunol. 147:1701-1708(1991).
RN [2]
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=9238663; PubMed=1517565;
RA Giordano R., Weisberg E.P., Ip T.K., Trucco M.;
RT "Genomic structure and strain-specific expression of the natural
RT killer cell receptor NKR-P1.";
RL J. Immunol. 149:1957-1963(1992).
CC -!- FUNCTION: May function as signal-transmitting receptor.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M77677; AAA39823.1; -.
DR EMBL; X64721; CAA45974.1; -.
DR PIR; B46467; B46467.
DR MGD; MGI:107539; KLR1b.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin c; 1.
DR PRINTS; PR00356; ANTIREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
FT DOMAIN 1 43
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 44 63
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 64 223
FT EXTRACELLULAR (POTENTIAL).
FT DISULFID 93 212
FT DISULFID 94 105
FT DISULFID 122 210
FT DISULFID 189 202
FT CARBOHYD 81 81
FT CARBOHYD 169 169
FT CARBOHYD 186 186
FT SEQUENCE 223 AA; 25157 MW; 8D04C11DEB9C56 CRC64;
Query Match
Score 149; DB 1; Length 223;


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CC      differentiated plasma cells.
CC      !- SIMILARITY: Contains 1 C-type lectin family domain.
CC      !- DATABASE: NAME=PROW; NOTE=CD guide CD72 entry;
CC      WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd72.htm".
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      use by non-profit institutions as long as its content is in no way
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M54992; AAA36189.1; -.
DR      EMBL; BC030227; AAH30227.1; -.
DR      PIR; A43532; A43532.
DR      Genew; HGNC:1696; CD72.
DR      MIM; 107272; -.
DR      GO; GO:0005102; F:receptor binding; TAS.
DR      GO; GO:0007155; P:cell adhesion; TAS.
DR      InterPro; IPR001304; Lectin C.
DR      Pfam; PF00059; lectin_c; 1.
DR      SMART; SM00034; CLECT; 1.
DR      PROSITE; PS00615; C-TYPE LECTIN 1; FALSE NEG.
DR      PROSITE; PS00411; C-TYPE LECTIN 2; 1.
KW      Antigen; Signal-anchor; Transmembrane; Lectin; Glycoprotein.
FT      DOMAIN          1   95
FT      TRANSMEM        96  116
FT      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT      (POTENTIAL).
FT      DOMAIN          117  359
FT      EXTRACELLULAR (POTENTIAL).
FT      DOMAIN          232  352
FT      C-TYPE LECTIN (LONG FORM).
FT      DISULFID        233  244
FT      BY SIMILARITY.
FT      DISULFID        261  350
FT      BY SIMILARITY.
FT      DISULFID        325  342
FT      BY SIMILARITY.
FT      CARBOHYD        136  136
FT      N-LINKED (GLCNAC...) (POTENTIAL).
SQ      SEQUENCE      359 AA; 40220 MW; 87A52C028AC17E44 CRC64;

Query Match          14.3%; Score 147.5; DB 1; Length 359;
Best Local Similarity 27.3%; Pred. No. 2.6e-07;
Matches 38; Conservative 19; Mismatches 61; Indels 21; Gaps 6;

QY      62 CGSKDSTCHPCSPILWTRNGSHCYFPMKKDWNSSLKFCADKGSLLTF---PDNQ 117
Db      ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db      226 CGSAD-TC-----CPSGWIMHOKSCFYISLTSKNWQESQKQCTLSKLATFSEIYPQSH 279

QY      118 GVKLFGEYL---GQDFYWGILRNIDGWRWEGGPPALSLRLTNSLIQRCGAIHRN---G 169
Db      : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY      280 SYFYFNSLLPNGSGNSYWTGLSSNKNWKLTD---TQRTTYAQSSCKNKVHKTWSWWT 336
Db      : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

QY      170 IQASSCEVALQWICKKVLV 188
Db      : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

Db      337 LESESCRSPLPYICEWTAF 355

Search completed: August 10, 2004, 16:17:00
Job time : 8.32035 secs
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:11:32 ; Search time 32.6089 Seconds

(without alignments)
1819.059 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029

Sequence: 1 MADSSYSLTELEPAQVQD.....GLQASCEVALQWICKKVLV 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1029	100.0	188	11	O88713
2	838	81.4	188	11	O64335
3	568.5	55.2	189	4	O75613
4	564.5	54.9	195	4	O96E93
5	548.5	53.3	189	4	O43198
6	182	17.7	257	13	Q90636
7	180.5	17.5	227	11	Q91V25
8	180	17.5	179	11	O54708
9	180	17.5	179	11	O54707
10	179.5	17.4	227	11	Q925G4
11	179.5	17.4	227	11	Q61973
12	177.5	17.2	179	6	Q8MH78
13	177	17.2	233	6	Q8MJH7
14	177	17.2	236	6	Q95L94
15	177	17.2	275	11	Q9D403
16	176	17.1	233	6	Q8MJH6

17	175	17.0	233	6	Q8MJ10
18	174.5	17.0	179	6	Q8MJ13
19	174.5	17.0	179	6	Q8MH19
20	174.5	17.0	200	6	Q8SPX1
21	174.5	17.0	231	6	Q9MZK3
22	173	16.8	231	6	Q8MI05
23	172	16.7	233	6	Q8MJH8
24	171.5	16.7	179	6	Q8MJ14
25	171.5	16.7	181	4	Q9NZS1
26	170.5	16.6	231	6	Q9GK88
27	169.5	16.5	200	13	Q802S8
28	169	16.4	159	6	Q8SPX0
29	168	16.3	165	11	Q9E007
30	168	16.3	233	6	Q8MJH5
31	168	16.3	233	6	Q8MJH9
32	167	16.2	233	6	Q8MJ11
33	167	16.2	246	6	Q9MZK2
34	166.5	16.2	231	4	Q9NZS2
35	165	16.0	246	6	Q9MZK1
36	164.5	16.0	225	4	Q12918
37	163.5	15.9	146	13	Q9IAM0
38	163.5	15.9	146	13	Q8JIW1
39	163.5	15.9	191	4	Q9UHP7
40	163	15.8	161	6	Q95JG4
41	162.5	15.8	233	6	Q9GME8
42	162.5	15.8	233	6	Q9MZ40
43	161.5	15.7	223	11	Q925G3
44	161.5	15.7	226	6	Q9MZ39
45	161.5	15.7	334	4	Q96QF9

ALIGNMENTS

RESULT 1

O88713 PRELIMINARY; PRT; 188 AA.
ID O88713
AC O88713;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-AUG-1999 (TREMBLrel. 11, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-like receptor G1).
DE like receptor G1).
GN KLRG1 OR MAFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C.B-17 SCID;
RX MEDLINE=99077194; PubMed=9862378;
RA Hanke T., Corral L., Vance R.E., Raulet D.H.;
RT "2F1 antigen, the mouse homolog of the rat 's1', is a lectin-like type II transmembrane receptor expressed by natural killer cells.";
RL Eur. J. Immunol. 28:4409-4417(1998).
RN [2]
RP SEQUENCE OF 2-188 FROM N.A.
RA Blaser C.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvevTACFB; TISSUE=Spleen;
RX MEDLINE=21115136; PubMed=11220622;
RA Voehringer D., Kaufmann M., Pircher H.;
RT "Genomic structure, alternative splicing, and physical mapping of the killer cell lectin-like receptor G1 gene (KLRG1), the mouse homologue of MAFA.";
RL Immunogenetics 52:206-211(2001).
DR EMBL; AF097357; AAD03718.1; -
DR EMBL; AJ010751; CAA09342.1; -
DR EMBL; AF317727; AAK40082.1; -
DR MGD; MGI:1355294; Klrp1.


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RESULT 4
Q96E93 PRELIMINARY; PRT; 195 AA.
AC Q96E93;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to killer cell lectin-like receptor subfamily G, member 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Strausberg R.;
RL SUBMITTED (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012621; AAH12621.1; -.
DR GenBank; HGNC:6380; KIRG1.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Receptor.
SQ SEQUENCE 195 AA; 21831 MW; 178EE98E08EEC473 CRC64;

Query Match 54.9%; Score 564.5; DB 4; Length 195;
Best Local Similarity 57.0%; Pred. No. 6.1e-51;
Matches 106; Conservative 25; Mismatches 54; Indels 1; Gaps 1;

QY 1 MADSSYSTLELPEAPQVQDESRLKAVLHRLPHLSRFAMVALGLLTIVILMLYQRI 60
DB 1 MTDVSIYSMLELTATQAQNDYGPQKSSSRSCSLVAIALGLITAVLLVLLQWIL 60
QY 61 CGSKDSTCHSCPILWTRNGSHCYFYSMEKDWNSLKPCADKSGHLLTFFDNGVK 120
DB 61 CGSNYSTCASCPCPDRAWKYGHCYFVSVEKDWNSLSLEFCLARDSHLLVITDQMS 120
QY 121 LFGEYLQDGYFWIGLNRIDGWEGGPAISL-RILTNSLIQRCGAIHNGLQASSCEVAL 179
DB 121 LLQVFSEAFQWIGLNRNSGWRWEDGSLNFSRISSNFVQTCGAINKGLQASSCEVPL 180
QY 180 QWICKK 185
DB 181 HWCKK 186

Query Match 54.9%; Score 564.5; DB 4; Length 195;
Best Local Similarity 57.0%; Pred. No. 6.1e-51;
Matches 106; Conservative 25; Mismatches 54; Indels 1; Gaps 1;

QY 1 MADSSYSTLELPEAPQVQDESRLKAVLHRLPHLSRFAMVALGLLTIVILMLYQRI 60
DB 1 MTDVSIYSMLELTATQAQNDYGPQKSSSRSCSLVAIALGLITAVLLVLLQWIL 60
QY 61 CGSKDSTCHSCPILWTRNGSHCYFYSMEKDWNSLKPCADKSGHLLTFFDNGVK 120
DB 61 CGSNYSTCASCPCPDRAWKYGHCYFVSVEKDWNSLSLEFCLARDSHLLVITDQMS 120
QY 121 LFGEYLQDGYFWIGLNRIDGWEGGPAISL-RILTNSLIQRCGAIHNGLQASSCEVAL 179
DB 121 LLQVFSEAFQWIGLNRNSGWRWEDGSLNFSRISSNFVQTCGAINKGLQASSCEVPL 180
QY 180 QWICKK 185
DB 181 HWCKK 186

RESULT 5
O43198 PRELIMINARY; PRT; 189 AA.
AC O43198;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mast cell function-associated antigen.
GN MAF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=96436735; PubMed=9765598;
RA Lamers M.B., Lamont A.G., Williams D.H.;
RT "Human MAF has alternatively spliced variants.";
RL Biochim. Biophys. Acta 1399:209-212 (1998).
DB EMBL; AF034952; AAC34731.1; -.

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DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0003793; F:defense/immunity protein activity; TAS.
DR GO; GO:0005530; F:lectin; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR GO; GO:0006968; P:cellular defense response; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 189 AA; 21079 MW; 15E042AD40B2B4F6 CRC64;

Query Match 53.3%; Score 548.5; DB 4; Length 189;
Best Local Similarity 55.8%; Pred. No. 2.8e-49;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 MADSSYSTLELPEAPQVQDESRLKAVLHRLPHLSRFAMVALGLLTIVILMLYQRI 60
DB 1 MTDVSIYSMLELTATQAQNDYGPQKSSSRSCSLVAIALGLITAVLLVLLQWIL 60
QY 61 CGSKDSTCHSCPILWTRNGSHCYFYSMEKDWNSLKPCADKSGHLLTFFDNGVK 120
DB 61 CGSNYSTCASCPCPDRAWKYGHCYFVSVEKDWNSLSLEFCLARDSHLLVITDQMS 120
QY 121 LFGEYLQDGYFWIGLNRIDGWEGGPAISL-RILTNSLIQRCGAIHNGLQASSCEVAL 179
DB 121 LLQVFSEAFQWIGLNRNSGWRWEDGSLNFSRISSNFVQTCGAINKGLQASSCEVPL 180
QY 180 QWICKK 186
DB 181 HGCKK 187

RESULT 6
Q90636 PRELIMINARY; PRT; 257 AA.
AC Q90636;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 17.5 protein.
GN 17.5.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=94164691; PubMed=8119728;
RA Bernot A., Zoorob R., Auffray C.;
RT "Linkage of a new member of the lectin supergene family to the chicken
RT Mlc genes.";
RL Immunogenetics 39:221-229 (1994).
DR EMBL; M88072; AAA48558.1; -.
DR PIR; I50146; I50146.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 257 AA; 28814 MW; C67EA483F4B85333 CRC64;

Query Match 17.7%; Score 182; DB 13; Length 257;
Best Local Similarity 28.7%; Pred. No. 8.6e-11;
Matches 48; Conservative 25; Mismatches 72; Indels 22; Gaps 6;

QY 32 RPHLSRFAMVALG---LLTIVILMLYQRI--CGSKDSTCHSCPILWTRNGSHCY 87

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Db      86 QNRRRLVCLVALSPVCMVLVALVAVILQRPSC--SPRPFSHV--CPNAWVGQKCY 141
QY      88 YFSMEKKDWSNLSKFCADKSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNIDG---WEWE 144
Db      142 YFSTESDWSNRSHCHRLGSLATLDTKEEMFNLQYQRPADRWIGLHRAEGDEHWTWA 201
QY      145 GGPALSLRLNLSLI-----QRCGAIHRNGLOASSCEVALQWICKK 185
Db      202 DGS-----FTNRPFELRGGRGRCAYLNGDGISSALCHSEKFEWVCSR 243

RESULT 7
Q91V25 PRELIMINARY; PRT; 227 AA.
AC Q91V25;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE NKR-PIA (Natural killer cell receptor protein NKR-PIA).
GN KLRB1A OR NKR-PIA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Plougastel B.F.M., Yokoyama W.M.;
RT "Mouse NKR-PIA gene, genomic structure.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=9248165; PubMed=10229823;
RA Kung S.K., Su R.C., Shannon J., Miller R.G.;
RT "The NKR-P1B gene product is an inhibitory receptor on SJL/J NK
cells.";
RL J. Immunol. 162:5876-5887(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kung S.K.P., Su R.C., Shannon J., Miller R.G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF285840; AAK83003.1; -.
DR EMBL; AF285839; AAK83003.1; JOINED.
DR EMBL; AF354262; AAK39102.1; -.
DR MGD; MGI:107540; Klrbl1a.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 227 AA; 25715 MW; CCB8324AE07FBB97 CRC64;

Query Match 17.5%; Score 180.5; DB 11; Length 227;
Best Local Similarity 26.5%; Pred. No. 1.1e-10;
Matches 57; Conservative 32; Mismatches 99; Indels 27; Gaps 7;

QY 1 MADSIYSTLELPEAPQVQDSRWKLKAVLHR-PHLGRFAM-----VALGLLTVILMSLLM 55
Db 1 MDTARVYGLPRPTPGAWHESPPLPDACRCPRSHRLALKSLCAGLILLVWTLIGMSV 60
QY 56 YQRIILC-----CG-----SKDSTCSHCPCFILLWTRNGSHCYFSMEKKDWSNLSK 101
Db 61 LVRVLIQPSIEKCVLVLQENLNKTTDCSAKLECPQDWLSHRDKCFHVSQVSNTWEEGLV 120
QY 102 FCADKGSLLTFPDNQGVKLFGEYLGQDF--YWIGLRNI-----DCWRWEGGPAIS---LRI 153
Db 121 DCDGKATMLIQDQEEELRFLDSIKEKYNFWIGLRYTLTMDNKKWINGSTLNSDLVKI 180
QY 154 LTNSLIQRCGAIHRNGLOASSCEVALQWICKVLY 188

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Db      181 TGDITENDSCRAISGDKVTFESCNSDNRWICQKELY 215

RESULT 8
Q54708 PRELIMINARY; PRT; 179 AA.
AC Q54708;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CD94.
GN KLRD1 OR CD94.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CB.17 SCID;
RX MEDLINE=9812458; PubMed=9464811;
RA Vance R.E., Tanamachi D.M., Hanke T., Raulat D.H.;
RT "Cloning of a mouse homolog of CD94 extends the family of C-type
lectins on murine natural killer cells.";
RL Eur. J. Immunol. 27:3236-3241(1997).
DR EMBL; AF030312; AAC28244.1; -.
DR MGD; MGI:1196275; Klrcl.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
SQ SEQUENCE 179 AA; 20809 MW; D59E1CBB63139E45 CRC64;

Query Match 17.5%; Score 180; DB 11; Length 179;
Best Local Similarity 31.8%; Pred. No. 9.2e-11;
Matches 57; Conservative 25; Mismatches 75; Indels 22; Gaps 9;

QY 22 SRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIILCGSKDST-----CSHCPSCP 76
Db 7 TRWELMSVIFGIK-CLEFLMVTLG---VLLINSFTIQITQSPSTTTVEFQEVSECCVCL 62
QY 77 ILWTRNGSHCYFSMEKKDWSNLSKFCADKSHLLTFPDNQGVKLFGEYLGQDFYWIGL- 135
Db 63 DKWVGHQNCYFISKEEKSWERSRDFCASONSSLQ--PQSRNELSFMNF-SQTFFWIGMH 120
QY 136 ----RNIDGWREGGPALSLRLTN-SLIQRCGAI---HRNGLOASSCEVALQWICKKV 186
Db 121 YSEKRN--AWLWEDGTVPKDLFPFEFSVIRPEHCIVYSPSKSVSAESCENKRYICKKL 177

RESULT 9
Q54707 PRELIMINARY; PRT; 179 AA.
AC Q54707;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE DE killer cell lectin-like receptor, subfamily D, member 1 (CD94).
GN KLRD1 OR CD94.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Vance R.E., Tanamachi D.M., Hanke T., Raulat D.H.;
RL Eur. J. Immunol. 27:0-0(1997).
RN [2]
RP SEQUENCE FROM N.A.

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QY 54 LMVORILC-----CG-----SKDSTCSHCPCPILWTRNGSHCYVFSMEKDWNS 99
Db 61 LV--RVLLQKSEIKCVYLQENLNKTYDCSAKLECPQDWLSHDKCFHSHVSNWTWEEG 118
QY 100 LKFCADKGGSHLLTFPDNGVKLFGEYLGQDF--YWIGLRNTI---DGRWEGGPALS---L 151
Db 119 LVDGCGKATMLIQDQELRLDLSIKEKYNFSWIGLRYYTLPDNWKWINGSTLNSDVL 178
QY 152 RLITNSLIQRCAGHRNGLQASSCEVALQWICKVLY 188
Db 179 KITDDTENDSCAALSGDKVTFPESCNSDRNRWICQKELY 215

RESULT 12
Q8MHY8 PRELIMINARY; PRT; 179 AA.
AC Q8MHY8;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Natural killer cell receptor.
GN POPY-CD94.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_taxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22072192; PubMed=12077248;
RA Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
RT "NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal
RT Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
RT with MHC-C.";
RL J. Immunol. 169:220-229(2002).
DR EMBL; AF470381; AAM78481.1; -.
DR EMBL; AF470382; AAM78482.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
KW Receptor.
SQ SEQUENCE 179 AA; 20550 MW; 6752CB8F182CFD73 CRC64;

Query Match 17.2%; Score 177.5; DB 6; Length 179;
Best Local Similarity 31.8%; Pred. No. 1.7e-10;
Matches 54; Conservative 16; Mismatches 69; Indels 31; Gaps 7;

QY 44 GLLTVILSLMYQRIICGS-----KSTCSHCPCPILWTRNGS 84
Db 14 GTLGILICLSMATGILKNSFTKLSIEPAFTPGPDIELOKSDC--C-SQCKWVGYYRC 70
QY 85 HCYVFSMEKDWNSLKFCDKGGSHLLTFPDNGVKLFGEYLGQDFYWIGLRNTI---GW 141
Db 71 NCYFISSEQKWTNRSRHLCAQKSSLLQIQWDELDFMSS--SQQFYWIGLSYSEHTAW 128

QY 142 RWEGGPALS---LRITLSLIQRCAGHRNG--LQASSCEVALQWICKVLY 187
Db 129 LWENGSAISQVLPFLPFTFNPKNCIAYPNENGALDESCECDKRYICKQQL 178

RESULT 13
Q8MJH7 PRELIMINARY; PRT; 233 AA.
AC Q8MJH7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Natural killer cell lectin-like receptor.
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GN POPY-NKG2A.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_taxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22072192; PubMed=12077248;
RA Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
RT "NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal
RT Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
RT with MHC-C.";
RL J. Immunol. 169:220-229(2002).
DR EMBL; AF470395; AAM78495.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
KW Receptor; Lectin.
SQ SEQUENCE 233 AA; 26239 MW; 6B8AE8489BAD2686 CRC64;

Query Match 17.2%; Score 177; DB 6; Length 233;
Best Local Similarity 24.5%; Pred. No. 2.6e-10;
Matches 48; Conservative 28; Mismatches 84; Indels 36; Gaps 6;

QY 7 YSTLELPEAPQVQDESRLKAVLHRPHLSFAMVALGLLTVILM-----SLLM 55
Db 59 YHKDLPSAPE-----KLIVGILGILCLVLMASVVTIWIPTLIQ 99
QY 56 YQRIILCGSKDSTCSHCPCPILWTRNGSHCYVFSMEKDWNSLKFCDKGGSHLLTFPD 115
Db 100 KHNSSSLNRTQKAHRCGHCPEWITVNSCYIYIGKERTWEESLLACASNSSLSDN 159
QY 116 NQGVKLFGEYLGQDFYWIGL--RNIDGFWFE--GGPALSLRILTNLSLIQ--CGAIHRNGLIQ 171
Db 160 EEMKFLGTILPSS--WIGVFNSSHPWVINGLAFQKEIKDSDNAEHDCAVLHTRGLR 217
QY 172 ASSCEVALQWICKVLY 187
Db 218 SNKCGSSILYHCKHKL 233

RESULT 14
Q95L94 PRELIMINARY; PRT; 236 AA.
AC Q95L94;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE NK2-F3.
GN NK2-F3.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_taxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA LaBonte M.L., Letvin N.L.;
RT "Analysis of rhesus monkey CD94/NKG2 family members.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF395617; AAK97464.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 236 AA; 26365 MW; 1987FAEF3641351E CRC64;
```



```
Query Match      17.2%; Score 177; DB 6; Length 236;
Best Local Similarity 25.0%; Pred. No. 2.6e-10;
Matches 47; Conservative 33; Mismatches 82; Indels 26; Gaps 7;

QY 20 DESRWKLVLRPHPLSRFAMVALGLTLVILMSLMYQRIL--CCG-----S 64
DB 55 NDKTYHCKGLGPP--EKLTAELVIGICIVLMATVLTKTVLIPICIGLEQNFSNLRIQ 112
QY 65 KDSCTCHCPCPILWTRNGSHCYFYSMEKDWNSSLKFCADKSHLLTFPDNQGVLFG 124
DB 113 KAYDCGHCPEWITYTNS---CYIYKREKTWEESLLTCAKNSLLSIDNEEMQLLGS 169
QY 125 YLQGDFFWIGLRNIDG--WRWEGGPALSLRIITNSL-IQRCGAIHNGLOASSCEVALQ 180
DB 170 L--SVLSWVGVSRSDDHPWVSINGSTFKLIAESDICKENCVMHLSSGLKSHRCASQL 227
QY 181 WICKVLY 188
DB 228 YTCKHKLW 235

RESULT 15
Q9D403
ID Q9D403 PRELIMINARY; PRT; 275 AA.
AC Q9D403;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 4933425B16RIK protein.
GN 4933425B16RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR ENBL; AK016908; BAB30491.1; -.
DR HSSP; P23807; IIXX.
DR MGD; MGI:1918433; 4933425B16RIK.
DR GO; GO:0005529; F-sugar binding; IEA.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
SQ SEQUENCE 275 AA; 31360 MW; C9792BA25C8B5CC2 CRC64;

Query Match      17.2%; Score 177; DB 11; Length 275;
Best Local Similarity 31.7%; Pred. No. 3.1e-10;
Matches 40; Conservative 17; Mismatches 57; Indels 12; Gaps 5;

QY 72 CPSCPILWTRNGSHCYFYSN-EKKDWNSSLKFCADKSHLLTFPDNQGVLFGYLGQ-- 128
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Db 139 CNPCPKTWQWYGNSCYFYSNEEKSWSDSRKOCIDKNATLVKIDSTEERLLQSLTF 198
QY 129 DFYWIGLR-NIDG--WRWEGGPALSLRIITNSLI-----QRCGAIHNGLOASSCEVAL 179
DB 199 SPFWLGLSWNSSGRNWLWEDGSPPTLLSDKELASFNGSRECAFYFERGNIYTSRCRAEI 258
QY 180 QWICKK 185
DB 259 PWICEK 264
```

Search completed: August 10, 2004, 16:18:49
Job time : 33.6089 secs

mis Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:05:01 ; Search time 46.5841 Seconds
(without alignments)
1140.281 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029

Sequence: 1 MADSSYISTLEPEAPQVQD.....GLQASCEVALQWICKVLY 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 29Jan04:*

1: geneseqp1980s:*

2: geneseqp1980s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	1029	100.0	188	4	AAE11760	AAE11760	Mouse mas
2	838	81.4	188	2	AAE11760	AAE11760	Mouse mas
3	838	81.4	188	2	AAE11760	AAE11760	Mouse mas
4	838	81.4	188	2	AAE11760	AAE11760	Mouse mas
5	568.5	55.2	189	7	ADD25635	ADD25635	Binding d
6	551	53.5	114	2	AAE11760	AAE11760	Partial s
7	548.5	53.3	189	2	AAE11759	AAE11759	Human mas
8	548.5	53.3	189	4	AAE11759	AAE11759	Human mas
9	420.5	40.9	843	4	ABG05451	ABG05451	Novel hum
10	267.5	26.0	191	6	ABJ37898	ABJ37898	NOVX prot
11	222.5	21.6	99	2	AAW88267	AAW88267	Human MAF
12	182	17.7	257	2	AAW85594	AAW85594	Chicken 1
13	178.5	17.3	179	2	AAW64791	AAW64791	Human Kp4
14	178.5	17.3	179	2	AAW40222	AAW40222	CD94. 7/1
15	178.5	17.3	179	8	ABE76965	ABE76965	Human pro
16	173.5	16.9	199	2	AAW85593	AAW85593	Human CD6
17	173.5	16.9	199	7	ADD25621	ADD25621	Binding d
18	173.5	16.9	199	7	ADD25621	ADD25621	Binding d
19	172.5	16.8	568	5	ABB80569	ABB80569	Human sbg
20	171.5	16.7	231	5	ABB81897	ABB81897	Human NKP
21	168	16.3	199	2	AAW84660	AAW84660	Murine CD
22	168	16.3	199	2	AAW85595	AAW85595	Mouse CD6
23	167.5	16.3	142	4	AAW80296	AAW80296	Human pro
24	167.5	16.3	142	6	ABG72616	ABG72616	Human cyt
25	167.5	16.3	160	4	AAW80302	AAW80302	Human pro

ALIGNMENTS

RESULT 1

AAE11760

ID AAE11760 standard; protein; 188 AA.

XX AAE11760;

XX AC

DT 18-DEC-2001 (first entry)

DE Mouse mast cell function associated antigen (MAFA) protein.

XX Mouse; pharmaceutical composition; mast cell function associated antigen;

KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;

KW immunosuppressive; cytostatic.

XX Mus sp.

XX Key

XX Location/Qualifiers

FT Domain

FT 64..188

FT /note="Extracellular domain"

XX WO200170805-A2.

XX 27-SEP-2001.

XX 16-MAR-2001; 2001WO-US008596.

XX 17-MAR-2000; 2000US-0190716P.

XX (GEMI-) GEMINI SCI INC.

XX Takahashi N, Mikayama T;

XX WPI; 2001-611482/70.

XX N-PSDB; AAD18735.

XX Pharmaceutical composition for treating tumor by stimulating cytotoxic

XX activity of natural killer cell or T-cell, comprises an agent that binds

XX to mast cell function-associated antigen ligand on target cell.

XX Example 1; Page 19; 49pp; English.

XX The present invention relates to a pharmaceutical composition comprising

XX an agent which specifically binds to a mast cell function associated

XX antigen (MAFA) ligand on a target cell, and prevents or inhibits natural

XX killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA

XX ligand and a pharmaceutically acceptable excipient. The invention is

XX useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA

XX binding to a ligand on a target cell, by contacting the pharmaceutical

Ram88815 Human imm
Aaul19820 Human nov
Abp48040 Human pol
Adc11002 Human pro
Aaul19659 Human nov
Abp47879 Human pol
Adc10841 Human ext
Adr58409 Human NOV
Aar65189 NK cell a
Rab68586 Human hOC
Add67552 Human Ly1
Ray94741 Human clo
Raul19650 Human nov
Adp47870 Human pol
Adc10832 Human ext
Rau27288 Human G52
Adc38664 Human sec
Aaw40219 Type II i
Ade07884 Novel pro
Raul19657 Human nov

26 166.5 16.2 198 4 RAM88815
27 166.5 16.2 198 4 AAU19820
28 166.5 16.2 198 5 ABP48040
29 166.5 16.2 198 7 ADC11002
30 166.5 16.2 203 4 AAU19659
31 166.5 16.2 203 5 ABP47879
32 166.5 16.2 203 7 ADC10841
33 166.5 16.2 345 6 ABR58409
34 164.5 16.0 225 2 AAR65189
35 163.5 15.9 191 4 AAB68586
36 163.5 15.9 191 7 ADD67552
37 163.5 15.9 272 3 RAY94741
38 162.5 15.8 251 4 AAU19650
39 162.5 15.8 251 5 ABP47870
40 162.5 15.8 251 7 ADC10832
41 160.5 15.6 181 2 AAU27288
42 160.5 15.6 181 7 ADC38664
43 160.5 15.6 231 2 AAW40219
44 160.5 15.6 241 7 ADE07884
45 160.5 15.6 265 4 AAU19657

CC composition in vitro, ex vivo or in vivo by administering the composition
CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
CC on the target cell. The agent or the composition is useful for treating a
CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
CC tumour cell. The invention is also useful for inhibiting an activity of
CC NK cell or a T-cell. The present sequence is mouse MAFA protein
XX
SQ Sequence 188 AA;

Query Match 100.0%; Score 1029; DB 4; Length 188;
Best Local Similarity 100.0%; Pred. No. 6.6e-103;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MADSSYSTLELPEAPQVQDSRWKLVKAVLHRLPHLSRFAMVALGLTIVLMSLLMYQRIL 60
DB 1 MADSSYSTLELPEAPQVQDSRWKLVKAVLHRLPHLSRFAMVALGLTIVLMSLLMYQRIL 60
QY 61 CCGSKDSTCSHCPCPIILWTRNGSHCYFVSMEKKDWNSSLKFCADKGSLLTFFPDNQGVK 120
DB 61 CCGSKDSTCSHCPCPIILWTRNGSHCYFVSMEKKDWNSSLKFCADKGSLLTFFPDNQGVK 120
QY 121 LFGEYLGQDFYWGILRNIDGWRWEGGPPALSRLITNSLIQRCGAHNRNGLOASSCEVALQ 180
DB 121 LFGEYLGQDFYWGILRNIDGWRWEGGPPALSRLITNSLIQRCGAHNRNGLOASSCEVALQ 180
QY 181 WICKKVL 188
DB 181 WICKKVL 188

RESULT 2

AAW77033
ID AAR77033 standard; protein; 188 AA.

AC AAR77033;

DT 01-FEB-1996 (first entry)

XX Mammalian mast cell function-associated antigen (MAFA).

XX Mast cell function-associated antigen; MAFA; soluble; ligand;
KW identification; screening; inflammation; inflammatory; allergy; allergic;
KW prevention.

XX Rattus rattus.

XX WO9527734-A1.

XX 19-OCT-1995.

XX 06-APR-1995; 95WO-US004258.

XX 08-APR-1994; 94IL-00109257.

XX (YEDA) YEDA RES & DEV CO LTD.
XX (RYCU/) RYCU S A.

XX Pecht I, Guthmann WD, Tal M;

XX WPI; 1995-366356/47.

XX N-PSDB; AAT01471.

XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -
PT useful for screening for ligands of MAFA which are useful for prevention
PT of inflammatory and allergic reactions.

XX Claim 12; Page 37; 54pp; English.

XX A soluble form of mast cell function-associated antigen (MAFA) can be
CC produced by recombinant techniques for use in the ligand- screening
CC assay. The ligands that are identified may be used alone or in

CC combination with the MAFA to prevent inflammatory and allergic reactions
XX
SQ Sequence 188 AA;

Query Match 81.4%; Score 838; DB 2; Length 188;
Best Local Similarity 80.7%; Pred. No. 3.2e-82;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADSSYSTLELPEAPQVQDSRWKLVKAVLHRLPHLSRFAMVALGLTIVLMSLLMYQRIL 60
DB 1 MADSSYSTLELPEAPQVQDSRWKLVKAVLHRLPHLSRFAMVALGLTIVLMSLLMYQRIL 60
QY 61 CCGSKDSTCSHCPCPIILWTRNGSHCYFVSMEKKDWNSSLKFCADKGSLLTFFPDNQGVK 120
DB 61 CCGSKGFMCSQCRCPNLWNRNGSHCYFVSMEKKDWNSSLKFCADKGSLLTFFPDNQGVN 120
QY 121 LFGEYLGQDFYWGILRNIDGWRWEGGPPALSRLITNSLIQRCGAHNRNGLOASSCEVALQ 180
DB 121 LFGEYVGEDFYWIGRIDGWRWEDGPALSRLITNSVYQCGTTHRCGLHASSCEVALQ 180
QY 181 WICKKVL 187
DB 181 WICKKVL 187

RESULT 3

AAW88277
ID AAW88277 standard; protein; 188 AA.

AC AAW88277;

DT 29-MAR-1999 (first entry)

XX Rat mast cell function-associated antigen (MAFA).

XX Mast cell function-associated antigen; MAFA; splice variant; rat;
KW inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.

XX Rattus sp.

XX Key Location/Qualifiers

FT Modified-site 82.84

FT /note= "Asn is N-glycosylated"

FT Modified-site 97.99

FT /note= "Asn is N-glycosylated"

XX WO9854209-A2.

XX 03-DEC-1998.

XX 29-MAY-1998; 98WO-GB001572.

XX 31-MAY-1997; 97GB-00011148.

XX (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX Hewitt EL, Lamers MBAC, Lamont A, Williams DH;

XX WPI; 1999-059806/05.

XX N-PSDB; AAW84222.

XX New polypeptide having a sequence corresponding to human mast cell
PT function-associated antigen - useful in forming and manufacturing
PT pharmaceutical compositions in the treatment of inflammatory and allergic
PT diseases, and tumour growth.

XX Disclosure; Fig 4; 44pp; English.

XX This is the amino acid sequence of rat mast cell function-associated
CC antigen (MAFA), a type II membrane glycoprotein found on mast cells and
CC basophils. The invention relates to cloning of the human MAFA molecule
CC (see AAW88265) and to the discovery of splice variants (see AAW88266-67)
CC of human MAFA that are not found in rat. Polypeptides and synthetic

XX The invention relates to a binding domain-immunoglobulin fusion protein
CC comprising a binding domain polypeptide that is fused to an
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC CH2 constant region polypeptide that is fused to the hinge region
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC polypeptide that is fused to the CH2 constant region polypeptide. The
CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC region polypeptide; derived from (a) having 3 or more cysteine residues;
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC contains 2 cysteine residues, where the first cysteine is not mutated; a
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC (a) having 3 or more cysteine residues, where the mutated human IgG1
CC immunoglobulin hinge region polypeptide contains no more than one
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC polypeptide, derived from (a) having 3 or more cysteine residues; where
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC capable of at least one immunological activity comprising antibody
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC binding domain polypeptide is capable of specifically binding to an
CC antigen. Also included are an isolated polynucleotide encoding the
CC binding domain-immunoglobulin fusion protein, a recombinant expression
CC construct comprising the polynucleotide (operably linked to a promoter),
CC a host cell transformed or transfected with a recombinant expression
CC construct, producing the binding domain-immunoglobulin fusion protein, a
CC pharmaceutical composition comprising the binding domain-immunoglobulin
CC fusion protein or polynucleotide and a carrier, and treating a subject
CC having or suspected of having a malignant condition or a B-cell disorder.
CC The binding domain-immunoglobulin fusion protein is useful for treating a
CC subject having or suspected of having a malignant condition or a B-cell
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC sclerosis or autoimmune disease. The present sequence is a binding domain
CC -immunoglobulin fusion protein-associated protein sequence. Note: The
CC sequence data for this patent formed part of the printed specification
CC and is also available in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC identified the sequences in the printed specification by their SEQ ID
CC number therefore none of the sequences can be explicitly identified.

XX SQ Sequence 189 AA;

Query Match 55.2%; Score 568.5; DB 7; Length 189;
Best Local Similarity 57.2%; Pred. No. 4.8e-53;
Matches 107; Conservative 25; Mismatches 54; Indels 1; Gaps 1;
QY 1 MADSIYSTLELPEAPQVQDSRWKIKAVLRPHLSRFAMVALGLLTVILMSLLMYQRIL 60
DB 1 MTDVSIYSMLPLPTATQNDYGPQKSSSRPSCSLVAIALGLLTAVLLSVLLYQWIL 60
QY 61 CCGSKDSTCSHCPCPIILWTRNGSHCYFYSMEKDWNSLKFCAKDGSHLLTFPDPNQVK 120
DB 61 CGGSNYSTCASCPCDPRWMYGNHCYFYSVEEKDWNSLEFCLARDSHLLVITDQMS 120
QY 121 LFGEYLGDQFYWIGLRNIDGWRWEGGPAISL-RILTNSLIQRCGATHRNGLOASSCEVAL 179
DB 121 LLOVFLSAFCWIGLRNNSGWRWEDGSPINFSRISNSFVQTCGAINKNGLOASSCEVPL 180
QY 180 OMICKKV 186
DB 181 HWVCKKV 187

RESULT 6

AAR77472
ID AAR77472 standard; protein; 114 AA.

XX AAR77472;

XX 01-FEB-1996 (first entry)

XX

DE Partial sequence of mast cell function-associated antigen (MAFA).
XX Mast cell function-associated antigen; MAFA; soluble; ligand;
KW identification; screening; inflammation; inflammatory; allergy; allergic;
KW prevention.
OS Rattus rattus.
PN WO9527734-A1.
XX 19-OCT-1995.
PF 06-APR-1995; 95WO-US004258.
XX 08-APR-1994; 94IL-00109257.
XX (YEDA) YEDA RES & DEV CO LTD.
PA (RYCU/) RYCUS A.
PI Pecht I, Guthmann MD, Tal M;
XX WPI; 1995-366356/47.
DR N-PSDB; AAT01471.
XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -
PT useful for screening for ligands of MAFA which are useful for prevention
PT of inflammatory and allergic reactions.
XX Disclosure; Page 38; 54pp; English.
XX A soluble form of mast cell function-associated antigen (MAFA) can be
CC produced by recombinant techniques for use in the ligand- screening
CC assay. The ligands that are identified may be used alone or in
CC combination with the MAFA to prevent inflammatory and allergic reactions
XX Sequence 114 AA;
SQ Query Match 53.5%; Score 551; DB 2; Length 114;
Best Local Similarity 84.1%; Pred. No. 1.9e-51;
Matches 95; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
QY 75 CPILWTRNGSHCYFYSMEKDWNSLKFCAKDGSHLLTFPDPNQVKLFGEYLGDQFYWIG 134
DB 1 CPILWTRNGSHCYFYSMEKDWNSLKFCAKDGSHLLTFPDPNQVKLFGEYLGDQFYWIG 60
QY 135 LRNIDGWRWEGGPAISL-RILTNSLIQRCGATHRNGLOASSCEVALQWICKKV 187
DB 61 LRNIDGWRWEDGPAISLSILNSVQKGTIHRCLHASSCEVALQWICKKV 113
RESULT 7
AAR88265
ID AAR88265 standard; protein; 189 AA.
XX AAR88265;
XX 29-MAR-1999 (first entry)
XX Human mast cell function-associated antigen (MAFA).
XX Mast cell function-associated antigen; MAFA; splice variant; human;
KW inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 7..10
FT Modified-site /note= "ITIM motif"
FT Modified-site 65..67
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site 97..99
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site 137..139

FT /note= "Asn is N-glycosylated"
 PT Modified-site 150..152
 FT /note= "Asn is N-glycosylated"
 XX
 PN WO9854209-A2.
 XX
 PD 03-DEC-1998.
 XX
 XX
 PF 29-MAY-1998; 98WO-GB001572.
 XX
 PR 31-MAY-1997; 97GB-00011148.
 XX
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
 XX
 XX Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
 XX WPI; 1999-059806/05.
 DR N-PSDB; AAV84198.
 XX
 PT New polypeptide having a sequence corresponding to human mast cell
 function-associated antigen - useful in forming and manufacturing
 PT pharmaceutical compositions in the treatment of inflammatory and allergic
 PT diseases, and tumour growth.
 XX
 PS Disclosure; Fig 1; 44pp; English.
 XX
 CC This is the amino acid sequence of human mast cell function- associated
 antigen (MAFA), a type II membrane glycoprotein. cDNA (see AAV84198)
 CC encoding human MAFA can be obtained from myelogenous leukaemic cell line
 CC K0912 or cDNA derived from human lung tissue. The encoded protein is
 CC similar to the rat form (see AAW88277) having an intracellular domain
 CC containing a putative immunoreceptor tyrosine activation motif (ITIM) and
 CC an extracellular lectin-like domain. 2. Alternatively spliced forms (see
 CC AAW8266-67) of human MAFA have been identified. Polypeptides and
 CC synthetic peptides (see AAW8258-64) based on these truncated MAFA
 CC proteins can be used in methods for the treatment of inflammatory and
 CC allergic diseases, and tumour growth
 XX
 SQ Sequence 189 AA;
 Query Match 53.3%; Score 548.5; DB 2; Length 189;
 Best Local Similarity 55.6%; Pred. No. 7e-51;
 Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;
 QY 1 MADSSLYSTLELPEAPQVQDESRLKAVLHRLHSLRFAMVALGLTLVILMSLLMYQRI 60
 Db 1 MTDVLYSMLELPTAQNDYGPQQKSSSSKSCSLVAITLGLTAVLLSVLLYQWIL 60
 QY 61 CCGSKDSTCSHCPCSPILWTRNGSHCYFYSMEKKDWNSSILKFCADKGSLLTTPDNQGVK 120
 Db 61 CQGSNYSTCASCPCSPDRWMKYGNHCYFYSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120
 QY 121 LFGEYLGQDPYWGILRNIDGWRWEGGPAISL-RILTNLSLQRCGAHRNGLQASCEVAL 179
 Db 121 LLQVFLSEAPFCWIGLRNNSGWRWEDGSPNFSRISNSFVQTCCGAINKNGLQASCEVPL 180
 QY 180 QWICKKV 186
 Db 181 HGVCKKV 187
 RESULT 8
 AAE11759
 ID AAE11759 standard; protein; 189 AA.
 XX
 AC AAE11759;
 XX
 XX 18-DEC-2001 (first entry)
 XX Human mast cell function associated antigen (MAFA) protein.
 XX Human; pharmaceutical composition; mast cell function associated antigen;
 KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
 KW

KW immunosuppressive; cytostatic.
 XX Homo sapiens.
 OS WO200170805-A2.
 PN 27-SEP-2001.
 PD
 XX
 PF 16-MAR-2001; 2001WO-US008596.
 XX
 PR 17-MAR-2000; 2000US-0190716P.
 XX
 PA (GEMI-) GEMINI SCI INC.
 XX
 XX Takahashi N, Mikayama T;
 PI WPI; 2001-611482/70.
 DR N-PSDB; AAD18734.
 XX
 PT Pharmaceutical composition for treating tumor by stimulating cytotoxic
 activity of natural killer cell or T-cell, comprises an agent that binds
 to mast cell function-associated antigen ligand on target cell.
 PT
 XX
 PS Claim 10; Page 18; 49pp; English.
 XX
 CC The present invention relates to a pharmaceutical composition comprising
 an agent which specifically binds to a mast cell function associated
 CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
 CC killer (NK) or T-cell-expressed cell surface MAFA from binding to MAFA
 CC ligand and a pharmaceutically acceptable excipient. The invention is
 CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
 CC binding to a ligand on a target cell, by contacting the pharmaceutical
 CC composition in vitro, ex vivo or in vivo by administering the composition
 CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
 CC on the target cell. The agent or the composition is useful for treating a
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
 CC tumour cell. The invention is also useful for inhibiting an activity of
 CC NK cell or a T-cell. The present sequence is human MAFA protein
 XX
 SQ Sequence 189 AA;
 Query Match 53.3%; Score 548.5; DB 4; Length 189;
 Best Local Similarity 55.8%; Pred. No. 7e-51;
 Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;
 QY 1 MADSSLYSTLELPEAPQVQDESRLKAVLHRLHSLRFAMVALGLTLVILMSLLMYQRI 60
 Db 1 MTDVLYSMLELPTAQNDYGPQQKSSSSKSCSLVAITLGLTAVLLSVLLYQWIL 60
 QY 61 CCGSKDSTCSHCPCSPILWTRNGSHCYFYSMEKKDWNSSILKFCADKGSLLTTPDNQGVK 120
 Db 61 CQGSNYSTCASCPCSPDRWMKYGNHCYFYSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120
 QY 121 LFGEYLGQDPYWGILRNIDGWRWEGGPAISL-RILTNLSLQRCGAHRNGLQASCEVAL 179
 Db 121 LLQVFLSEAPFCWIGLRNNSGWRWEDGSPNFSRISNSFVQTCCGAINKNGLQASCEVPL 180
 QY 180 QWICKKV 186
 Db 181 HGVCKKV 187
 RESULT 9
 ABG05451
 ID ABG05451 standard; protein; 843 AA.
 XX
 AC ABG05451;
 XX
 XX 13-FEB-2002 (first entry)
 XX Novel human diagnostic protein #5442.
 DE

```

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX N-PSDB; AAS69638.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID NO 35810; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 843 AA;
XX
Query Match 40.9%; Score 420.5; DB 4; Length 843;
Best Local Similarity 50.3%; Pred. No. 3.7e-36;
Matches 80; Conservative 26; Mismatches 52; Indels 1; Gaps 1;
QY 11 ELPEAPQVQDSRWKLVKAVLRPHLSRFAMVALGLTTLVLMQLYQILCGSKDSTCS 70
D6 665 ELPTATQNDYGPQKSSSRPSCSLVALAGLLTAVLLSVLYQILCGSNYSTCA 724
QY 71 HCPSCPILWTRNGSHCYFYSMEKDWNSSLKPCADKGSLLTFFPDNQGVKLFGEYIGQDF 130
D6 725 SCSPCFDRWKNYGNHYFYSVEEKDWNSLSEFCLARDSHLLVITDQEMSLQLVFLSEAF 784
QY 131 YWIGLRNIDGWREGGPALSLRLTN-SLIQRCGAHNR 168
D6 785 CWIGLRNNSGMWEDGSLNFRNTNGTIIRKRHLHXN 823
XX
RESULT 10
ABU37898
ID ABU37898 standard; protein; 191 AA.

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XX AC ABU37898;
XX
XX 22-MAY-2003 (first entry)
XX
XX NOVX protein sequence SEQ ID No 42.
XX
XX Hepatotropic; immunosuppressive; cardiant; hypertensive; tranquilizer;
KW vulnerary; virucide; antibacterial; protozoacide; fungicide; nootropic;
KW antiparasitic; neuroprotective; cerebroprotective; antiparkinsonian;
KW anticonvulsant; antiaddictive; analgesic; dermatological; keratolytic;
KW antiseborrheic; antiarthritis; antiarthritic; antinflammatory; anti-HIV;
KW cytostatic; antiasthmatic; antipsoriatic; hypotensive; osteopathic;
KW antitumor; anorectic; antidiabetic; antiallergic; haemostatic;
KW neuroleptic; antidepressant; antiinfertility; NOVX; human disease;
KW NOVX-associated disorder; trauma; viral; bacterial; fungal; protozoal;
KW parasitic infection; Alzheimer's disease; stroke; forensic biology;
KW immunogen; non-human transgenic animal; gene therapy.
XX
XX Unidentified.
XX
XX WO200281517-A2.
XX
XX 17-OCT-2002.
XX
XX 22-JAN-2002; 2002WO-US002064.
XX
XX 19-JAN-2001; 2001US-0262892P.
XX
XX 23-JAN-2001; 2001US-0263598P.
XX
XX 24-JAN-2001; 2001US-0283799P.
XX
XX 25-JAN-2001; 2001US-0264117P.
XX
XX 26-JAN-2001; 2001US-0264139P.
XX
XX 30-JAN-2001; 2001US-0264478P.
XX
XX 02-MAR-2001; 2001US-0263351P.
XX
XX 14-MAR-2001; 2001US-0275927P.
XX
XX 15-MAR-2001; 2001US-0276449P.
XX
XX 23-MAR-2001; 2001US-0277358P.
XX
XX 29-MAR-2001; 2001US-0278151P.
XX
XX 20-APR-2001; 2001US-0285140P.
XX
XX 20-APR-2001; 2001US-0285141P.
XX
XX 30-APR-2001; 2001US-0287484P.
XX
XX 17-MAY-2001; 2001US-0291701P.
XX
XX 08-JUN-2001; 2001US-0296960P.
XX
XX 10-JUL-2001; 2001US-0304353P.
XX
XX 10-JUL-2001; 2001US-0304355P.
XX
XX 12-JUL-2001; 2001US-0304886P.
XX
XX 09-AUG-2001; 2001US-0311289P.
XX
XX 13-AUG-2001; 2001US-0311975P.
XX
XX 16-AUG-2001; 2001US-0312937P.
XX
XX 18-OCT-2001; 2001US-0330227P.
XX
XX 29-NOV-2001; 2001US-0334198P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Decristofaro MF, Padigar M, Miller C, Tchernev V, Zhong H;
XX Zhong M, Anderson D, Ballinger R, Gerlach V, Spytek KA, Rastelli L;
XX Kekuda R, Guo X, Zerhusen B, Andrew D, Mezes P, Patturajan M;
XX Burgess CE, Eisen A, Wolenc A, Baumgartner J, Shinkets RA, Gusev V;
XX Vernet CAM, Taupier R, Pena C, Shenoy S, Li L, Casman S, Boldog F;
XX Fernandes E, Smithson G, Malyankar U, Tallon B, Liu X;
XX
XX WPI; 2003-058504/05.
XX
XX N-PSDB; ABT33363.
XX
XX New polypeptides, designated as NOVX, useful for diagnosing and treating
PT infections, neurological diseases, cancer, allergy, and bone,
PT immunological, skin, renal, brain, muscle and autoimmune disorders.
XX
XX Claim 1; Page 118; 672pp; English.
XX

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CC The invention relates to a novel isolated polypeptide, designated NOVX
 CC (NOV1 - 33), consisting of a mature form of one of 61 sequences, given in
 CC the specification, or its variant, where amino acid residue(s) in the
 CC variant differ from the mature form, provided that the variant differs in
 CC not more than 15 % of the amino acids from the sequence of the mature
 CC form. The NOVX polypeptides, nucleic acids encoding the polypeptides, and
 CC an antibody to the polypeptides, are useful for treating or preventing a
 CC NOVX-associated disorder in humans and for treating a syndrome associated
 CC with a human disease (NOVX-associated disorder). NOVX polypeptides and
 CC the encoding nucleic acids, are useful for determining the presence of or
 CC predisposition to a disease associated with altered levels of NOVX
 CC polypeptide and polynucleotide, by measuring the level of polypeptide
 CC expression or the amount of nucleic acid from a mammal and comparing it
 CC with another mammal not having or not predisposed to the disease. NOVX
 CC polypeptide is also useful for identifying an agent that binds to NOVX
 CC and a cell expressing NOVX is useful for identifying an agent that
 CC modulates the expression or activity of NOVX. The antibodies and a
 CC polypeptide having 95 % sequence identity to NOVX polypeptide are useful
 CC for treating a pathological state in a mammal. The antibodies are also
 CC useful for determining the presence or amount of NOVX in a sample. NOVX
 CC polypeptides, polynucleotides and antibodies specific for the
 CC polypeptides are useful for treating or preventing disorders or syndromes
 CC including trauma, viral, bacterial, fungal, protozoal, and parasitic
 CC infections. They can also treat disorders such as e.g., Alzheimer's
 CC disease or a stroke. The NOVX encoding nucleic acids are useful for
 CC expressing the NOVX proteins, to detect NOVX mRNA, or a genetic lesion in
 CC a NOVX gene and to modulate NOVX activity. NOVX sequences are also useful
 CC for identifying a cell or tissue type in a biological sample, to amplify
 CC DNA sequences from very small biological samples such as tissues e.g.
 CC hair or skin or body fluids in forensic biology and as primers and probes
 CC for use in identifying and/or cloning NOVX homologues in other cell
 CC types. The NOVX proteins are useful as an immunogen to generate
 CC antibodies which are useful for diagnostically monitoring protein levels
 CC and modulating NOVX activity. Cells comprising NOVX nucleic acids are
 CC useful for producing non-human transgenic animals which are useful for
 CC studying the function and/or activity of NOVX protein and for identifying
 CC and/or evaluating modulators of NOVX protein activity. The NOVX nucleic
 CC acids can be used in gene therapy. This sequence represents a NOVX
 CC protein of the invention

XX SQ Sequence 191 AA;

Query Match 26.0%; Score 267.5; DB 6; Length 191;
 Best Local Similarity 31.2%; Pred. No. 1.9e-20;
 Matches 59; Conservative 27; Mismatches 80; Indels 23; Gaps 4;
 QY 12 LPEAPQVQDESRLKXAVLRPHLS-----RFAMVALGLLTVILSLMYQRIILCCGSKDS 67
 DB 12 LPESQPFESHQRLVLLPIL-BIHVNSKSYRMYSFCLGLTLVTRQSLALSPLECSGALSA 70
 QY 68 TCSHCPCSPILWTRNGSHCYFYSMEKDWNSLKFCDKGSLLITFPDNGVKLFGVILG 127
 DB 71 HCKICEPCPTSWLPFGGSCYFYSFKTTWBAQGHCDASAHAAFPEDRKVAFYSVLLG 130
 QY 128 QDFYWGILNRDGRWEGGPPALSRLITNSLIQRCGAIHR-----NGLQASSCEVA 178
 DB 131 RCLFGIGLARGVGRWQVAPGTQI-----DAPAVGQACFCQBSISGLPASELRLE 181
 QY 179 LQWICKVKYL 187
 DB 182 KWHCSKTL 190

RESULT 11

AAW88267
 ID AAW88267 standard; protein; 99 AA.

XX AC AAW88267;

XX DT 29-MAR-1999 (first entry)

XX DE Human MAFa splice variant huMAFA(E3/4-).

KW Mast cell function-associated antigen; MAFa; huMAFA(E3/4-);
 KW splice variant; human; inflammation; allergy; asthma;
 KW rheumatoid arthritis; tumour; therapy.

OS Homo sapiens.

PN WO9854209-A2.

XX PD 03-DEC-1998.

XX PF 29-MAY-1998; 98WO-GB001572.

XX PR 31-MAY-1997; 97GB-00011148.

XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX PI Hewitt EL, Lamers MBAC, Lamont A, Williams DH;

XX DR WPI; 1999-059806/05.

XX DR N-PSDB; AAV84200.

XX PT New polypeptide having a sequence corresponding to human mast cell
 PT function-associated antigen - useful in forming and manufacturing
 PT pharmaceutical compositions in the treatment of inflammatory and allergic
 PT diseases, and tumour growth.

XX PS Disclosure; Fig 3; 44pp; English.

XX CC This is the amino acid sequence of human mast cell function- associated
 CC antigen (MAFA) splice variant huMAFA(E3/4-), which lacks the C-lectin-
 CC like domain of human MAFa (see AAW88265) but retains the intracellular
 CC and transmembrane domains as well as the extracellular C-terminal tail.
 CC Truncated MAFa polypeptides including huMAFA(E3/4-), and polynucleotides
 CC encoding them, as well as synthetic peptides (see AAW88258-64, AAW88268-
 CC 72), can be used in compositions for the treatment of
 CC inflammatory and allergic diseases (e.g. rheumatoid arthritis and
 CC asthma), or tumour growth

XX SQ Sequence 99 AA;

Query Match 21.6%; Score 222.5; DB 2; Length 99;
 Best Local Similarity 30.1%; Pred. No. 5.9e-16;
 Matches 56; Conservative 13; Mismatches 28; Indels 89; Gaps 1;
 QY 1 MADSIYSTELEPEAPQVQDESRLKXAVLRPHLSRFAMVALGLLTVILSLMYQRIIL 60
 DB 1 MTDSVIYSMELEPTATQANDYGPQQKSSSRFSCSCLVAIALGLLTVALLVLLYQWIL 60
 QY 61 CCGSKDSTCSHCPCSPILWTRNGSHCYFYSMEKDWNSLKFCDKGSLLITFPDNGVK 120
 DB 61 CCG-----
 QY 121 LFGEYLGQDFYTWIGLRNIDGRWEGGPPALSRLITNSLIQRCGAIHRNGLQASSCEVALQ 180
 DB 64 -----ISSNSFVTCGATKNGLQASSCEVPLH 91
 QY 181 WICKKV 186
 DB 92 WICKKV 97

RESULT 12

AAW85594
 ID AAW85594 standard; protein; 257 AA.

XX AC AAW85594;

XX DT 17-OCT-2003 (revised)

XX DT 02-MAR-1999 (first entry)

XX DE Chicken 17.5.3 protein.

XX KW lectin; carbohydrate; binding; agglutination; selectin; receptor;

KW calcium dependent binding; treatment; cancer; detection; identification;
 KW CTL-1; ovary; paraganglionic; penis; brain; thyroid; heart.
 OS Gallus gallus.
 PN WO9849306-A1.
 XX
 PD 05-NOV-1998.
 XX
 PF 29-APR-1998; 98WO-US008791.
 XX
 PR 29-APR-1997; 97US-00846523.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX Bandman O, Shah P;
 PI
 XX WPI; 1999-024060/02.
 DR N-PSDB; AAV83109.
 DR
 XX New human C-type lectin and related nucleic acid, vectors, transformed
 PT cells - antibodies, agonists and antagonists, for diagnosis, prevention
 PT and treatment of cancers.
 PS
 XX Example 3; Page 48-49; 64pp; English.
 XX Chicken 17.5.3 protein shows homology with the human CTL-1 protein.
 CC Recombinant cells containing expression vectors comprising the CTL-1
 CC coding sequence can be used to produce recombinant CTL-1 which is useful
 CC for raising Ab and to screen for specific binding agents. Binding agents
 CC which are antagonists of CTL-1 can be used to treat or prevent cancer,
 CC e.g. of ovary, paraganglion, penis, brain, thyroid and heart which are
 CC associated with overexpression of CTL-1. Fragments of this sequence are
 CC used to diagnose these conditions, as probes or primers in usual
 CC hybridisation and/or amplification assays, or for gene mapping, while
 CC complements of this sequence, antisense or ribozyme sequences are used to
 CC treat or prevent the aforementioned cancers also. Ab are used directly as
 CC antagonists or for delivery of therapeutic agents to cells that express
 CC CTL-1. CTL-1 includes a carbohydrate-recognition domain (aa35-149) and
 CC also a transmembrane domain, but no secretory signal. CTL-1 also shows
 CC homology with human CD69 (AAW85593), and mouse CD69 (AAW85595) proteins.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 257 AA;
 Query Match 17.7%; Score 182; DB 2; Length 257;
 Best Local Similarity 28.7%; Pred. No. 5.1e-11;
 Matches 48; Conservative 25; Mismatches 72; Indels 22; Gaps 6;
 QY 32 RPHLSRFAMVALG----LLTVILMSLLMYQRIKCGSKDSTCSHCPCPILWTRNGSHCY 87
 Db RQNRRLVLCVALSAVPCMLVALVAVIVLQRPSC--SPRPFSHV--CFNAWVGFGKCY 141
 QY 88 YFSMEKDWNSLKFCAKDGSHLLTFPDNQVKLFGEYLGQDFYVIGLRNIDG---WWE 144
 Db YFSTESDWNSSREHCHRLGSLATLDTKEEMFLQYCRPADRWIGLHRAEGDEHWTWA 201
 QY 145 GGPALSLRILNLSII-----QRCGAIRHNGLOASSCEVALQWICKK 185
 Db 202 DGS-----FTNRPVFEELGGRCAYLNGDGISSALCHSEKFWVCSR 243
 RESULT 13
 AAW64791
 ID AAW64791 standard; protein; 179 AA.
 XX
 AC AAW64791;
 XX
 DT 23-NOV-1998 (first entry)
 XX
 DE Human Kp43 protein.
 XX
 KW Kp43; human; natural killer cell surface antigen; NK; T cell; inhibitor;

KW cell-mediated cytotoxicity; transplant rejection; autoimmune disease.
 XX Homo sapiens.
 XX US5811284-A.
 PN
 XX 22-SEP-1998.
 PD
 XX 20-MAY-1996; 96US-00650578.
 PF
 XX 29-DEC-1993; 93US-00175339.
 PR
 XX (SCHE) SCHERING CORP.
 PA (LOPE/) LOPEZ-BOTET M.
 PA (BELT/) BELTRAN J A.
 XX
 PI Lanier LL, Chang C, Lopez-Botet M, Beltran JA, Phillips JH;
 DR WPI; 1998-530877/45.
 DR N-PSDB; AAV46476.
 DR
 XX DNA encoding natural killer cell surface antigen Kp43 - and transformed
 PT cells for producing recombinant Kp43.
 PT
 XX Claim 1; Col 31-32; 17pp; English.
 PS
 XX This sequence represents a novel human natural killer (NK) cell surface
 CC antigen, Kp43. This sequence can be used in a method resulting in the
 CC production of recombinant protein expressed by NK and T cells, which may
 CC inhibit cell-mediated cytotoxicity, e.g. in transplant rejection or
 CC autoimmune diseases, or may be used to produce antibodies for diagnostic
 CC or therapeutic use
 XX
 SQ Sequence 179 AA;
 Query Match 17.3%; Score 178.5; DB 2; Length 179;
 Best Local Similarity 31.8%; Pred. No. 7.5e-11;
 Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;
 QY 44 GLLIVILMSLLMYQRIKCGS-----KSTCSHCPCPILWTRNGS 84
 Db GTLGIICLSMATILGILKNSFTKLSTPEAFTPGENTLQKSDC--C-SCQEKWVG YRC 70
 QY 85 HCYVFSMEKDWNSLKFCAKDGSHLLTFPDNQVKLFGEYLGQDFYVIGLRNIDG---GW 141
 Db NCYFISSEOKTWNSRHLCAQSKSLQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128
 QY 142 RWEGGPALSLRILTN---SLIQRCAIRHNG-LOASSCEVALQWICKKVL 187
 Db 129 LWENGSAISQYLFPSFETFKNCIAYNPNGNALDESCEDKNRYICKQOL 178
 RESULT 14
 AAW40222
 ID AAW40222 standard; peptide; 179 AA.
 XX
 AC AAW40222;
 XX
 DT 07-JUL-1998 (first entry)
 XX
 DE CD94.
 XX
 KW TMAH; apoptosis; osteoarthritis; diagnosis; treatment.
 XX
 OS Homo sapiens.
 XX WO9804585-A2.
 PN
 PD 05-FEB-1998.
 XX
 PF 22-JUL-1997; 97WO-US013077.
 XX
 PR 31-JUL-1996; 96US-00690095.

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XX PA (INCY-) INCYTE PHARM INC.
XX PI Hillman JL, Au-Young J, Goli SK;
XX XX WPI; 1998-130617/12.
XX DR Human macrophage antigen - used for decreasing apoptosis associated with
XX PT osteoarthritis.
XX PT Human macrophage antigen - used for decreasing apoptosis associated with
XX PT osteoarthritis.
XX PS Disclosure; Page 47; 58pp; English.
XX XX
XX CC The type II integral membrane proteins (AAW40219-W40221) and CD94
XX CC (AAW40222) form a group which has 20% homology with the human macrophage
XX CC antigen (TMAH) (AAW40215). The homology which TMAH shares with this group
XX CC includes a series of disulphide residues. The structural homology between
XX CC the peptides provides information on the structural and physical
XX CC properties of both the TMAH gene and protein. This is used in the
XX CC development of TMAH as a diagnostic tool and as a method of treating
XX CC diseases associated with expression of TMAH
XX XX
XX SQ Sequence 179 AA;
XX
Query Match 17.3%; Score 178.5; DB 2; Length 179;
Best Local Similarity 31.8%; Pred. No. 7.5e-11;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;
QY 44 GLLTVILMSLLMYQRIILCCGS-----KSTCSHCPCSPILWTRNGS 84
Db 14 GTLGIICLSMATLGIILLKNSFTKLSIEPAFTPCPNIELQKSDC--C-SCQEKWVGRC 70
QY 85 HCYYFSMEKDMNSSLKFCADKSGHLLTTPDNQGVKLFGEYLGQDFWIGLRNID---GW 141
Db 71 NCYFISSEQKTWNEHRHLCAQSKSLQLQNTDELDFMSS--SQQFYWIGLSYEHTAW 128
QY 142 RWEGGPALSRLITN---SLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
Db 129 LWENGSAQLPFPSPFTFTKNCIAYNPNGNALDESCEDKNRYICKQQL 178

RESULT 15
ADE76965
ID ADE76965 standard; protein; 179 AA.
XX AC
XX AC ADE76965;
XX DT
XX DT 29-JAN-2004 (first entry)
XX DE Human protein expressed in a liver disorder #36.
XX XX
XX KW human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
XX KW tumour; liver; inflammatory disorder; immune response disorder;
XX KW high-throughput screening; differential gene expression; gene therapy.
XX XX
XX OS Homo sapiens.
XX XX
XX XX US2003108871-A1.
XX XX
XX XX 12-JUN-2003.
XX XX
XX XX 30-JUL-2001; 2001US-00919039.
XX XX
XX XX 28-JUL-2000; 2000US-0222113P.
XX XX
XX XX (KASE/) KASER M R.
XX XX
XX XX Kaser MR;
XX XX
XX XX WPI; 2004-031227/03.
XX XX
XX XX N-PSDB; ADE76964.
XX XX
XX PT Composition comprising several cDNAs that are differentially expressed in
XX PT treated human C3A liver cell cultures, useful for treating liver

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PT disorders.
XX Claim 1; SEQ ID NO 130; 41pp; English.
XX
XX CC The invention relates to a composition comprising several cDNAs that are
XX CC differentially expressed in a liver disorder. The composition is useful
XX CC for treating liver disorder such as hyperlipidaemia, hypertension, type
XX CC II diabetes, tumours of the liver and disorders of the inflammatory and
XX CC immune response. The composition is useful for a high-throughput method
XX CC of screening several molecules or compounds to identify a ligand which
XX CC specifically binds a cDNA. A protein encoded by the cDNA is useful for a
XX CC high-throughput method for using a protein to screen several molecules or
XX CC compounds to identify at least one ligand which specifically binds the
XX CC protein which involves combining the protein encoded by the cDNA with
XX CC several of molecules or compounds under conditions to allow specific
XX CC binding, and detecting specific binding between the protein and a
XX CC molecule or compound, therefore identifying a ligand which specifically
XX CC binds the protein. The composition is useful for detecting and
XX CC quantifying differential gene expression, can be used in gene therapy, to
XX CC formulate prognosis and to design a treatment regimen and to monitor the
XX CC efficacy of treatment. The present sequence represents the amino acid
XX CC sequence of a protein encoded by a cDNA differentially expressed in a
XX CC liver disorder.
XX
XX SQ Sequence 179 AA;
XX
Query Match 17.3%; Score 178.5; DB 8; Length 179;
Best Local Similarity 31.8%; Pred. No. 7.5e-11;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;
QY 44 GLLTVILMSLLMYQRIILCCGS-----KSTCSHCPCSPILWTRNGS 84
Db 14 GTLGIICLSMATLGIILLKNSFTKLSIEPAFTPCPNIELQKSDC--C-SCQEKWVGRC 70
QY 85 HCYYFSMEKDMNSSLKFCADKSGHLLTTPDNQGVKLFGEYLGQDFWIGLRNID---GW 141
Db 71 NCYFISSEQKTWNEHRHLCAQSKSLQLQNTDELDFMSS--SQQFYWIGLSYEHTAW 128
QY 142 RWEGGPALSRLITN---SLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
Db 129 LWENGSAQLPFPSPFTFTKNCIAYNPNGNALDESCEDKNRYICKQQL 178

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Search completed: August 10, 2004, 16:16:28
Job time : 47.5841 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2004, 16:18:53 ; Search time 40.2619 Seconds
(without alignments)
1464.718 Million cell updates/sec

Title: US-09-811-367B-3
Perfect score: 1029
Sequence: 1 MADSSYSTLELPEAPQVD.....GLQASCEVALQWICKKVLX 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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2: /cgn2_6/ptodata/2/pubaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/2/pubaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubaa/US08_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/2/pubaa/US09A_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubaa/US10B_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/2/pubaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	838	81.4	188	9	US-09-811-367B-5
3	568.5	55.2	189	14	US-10-207-655-196
4	548.5	53.3	189	9	US-09-811-367B-1
5	182	17.7	257	14	US-10-179-528-4
6	178.5	17.3	179	10	US-09-919-039-130
7	178.5	17.3	179	15	US-10-335-009-10
8	173.5	16.9	199	10	US-09-284-320-86
9	173.5	16.9	199	14	US-10-207-655-182
10	173.5	16.9	199	14	US-10-179-528-3
11	173.5	16.9	199	15	US-10-379-127-26
12	171.5	16.7	231	16	US-10-451-843-1
13	170	16.5	546	12	US-10-072-012-158
14	170	16.5	549	12	US-10-072-012-160
15	168	16.3	199	14	US-10-179-528-7

16	166.5	16.2	198	9	US-09-764-870-470	Sequence 470, App
17	166.5	16.2	198	14	US-10-125-540-470	Sequence 470, App
18	166.5	16.2	203	9	US-09-764-870-309	Sequence 309, App
19	166.5	16.2	203	14	US-10-125-540-309	Sequence 309, App
20	166.5	16.2	345	15	US-10-262-839-94	Sequence 94, Appl
21	164.5	16.0	225	15	US-10-379-127-25	Sequence 25, Appl
22	163.5	15.9	191	15	US-10-335-009-2	Sequence 2, Appl
23	163.5	15.9	191	15	US-10-379-127-23	Sequence 23, Appl
24	162.5	15.8	251	9	US-09-764-870-300	Sequence 300, App
25	162.5	15.8	251	9	US-10-125-540-300	Sequence 300, App
26	160.5	15.6	181	13	US-10-114-893-22	Sequence 22, Appl
27	160.5	15.6	265	9	US-09-764-870-307	Sequence 307, App
28	160.5	15.6	265	14	US-10-125-540-307	Sequence 307, App
29	160.5	15.6	275	15	US-10-161-493-20	Sequence 20, Appl
30	156	15.2	182	9	US-09-764-870-310	Sequence 310, App
31	156	15.2	182	14	US-10-125-540-310	Sequence 310, App
32	156	15.2	268	15	US-10-161-493-22	Sequence 22, Appl
33	154	15.0	165	10	US-09-759-130B-98	Sequence 98, Appl
34	154	15.0	165	16	US-10-741-790-98	Sequence 88, Appl
35	154	15.0	190	10	US-09-759-130B-88	Sequence 88, Appl
36	154	15.0	190	16	US-10-741-790-88	Sequence 14, Appl
37	154	15.0	190	16	US-10-775-640-14	Sequence 4, Appl
38	153	14.9	316	9	US-09-862-802-4	Sequence 4, Appl
39	152.5	14.8	319	15	US-10-138-588-90	Sequence 90, Appl
40	152.5	14.8	1479	12	US-09-918-715-305	Sequence 305, App
41	152	14.8	189	9	US-09-764-870-487	Sequence 487, App
42	152	14.8	189	14	US-10-125-540-487	Sequence 487, App
43	151.5	14.7	399	16	US-10-451-459-2	Sequence 2, Appl
44	151	14.7	132	15	US-10-335-009-4	Sequence 4, Appl
45	149.5	14.5	1479	12	US-09-918-715-238	Sequence 238, App

ALIGNMENTS

RESULT 1

US-09-811-367B-3
; Sequence 3, Application US/09811367B
; Patent No. US2002015510A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US2002015510A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THE
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811.367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-811-367B-3

Query Match	100.0%	Score	1029;	DB	9;	Length	188;
Best Local Similarity	100.0%	Pred. No.	7.9e-101;				
Matches	188;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	MADSSYSTLELPEAPQVDSRWKLVKAVLRPHLSRFAMVAGLLTIVILMSLMYQRIIL	60				
Db	1	MADSSYSTLELPEAPQVDSRWKLVKAVLRPHLSRFAMVAGLLTIVILMSLMYQRIIL	60				
QY	61	CGGSKDSTCSHCPCPIILWTRNGSCYFYFSMEKDDNSLKFCDKDGSHLLTFPDNQGVK	120				
Db	61	CGGSKDSTCSHCPCPIILWTRNGSCYFYFSMEKDDNSLKFCDKDGSHLLTFPDNQGVK	120				
QY	121	LFGEYLGDQFYWIGLRNIDGWRWEGGPPALSRLILNSLIQRCGAHNRNGLOASCEVALQ	180				
Db	121	LFGEYLGDQFYWIGLRNIDGWRWEGGPPALSRLILNSLIQRCGAHNRNGLOASCEVALQ	180				

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QY      181 WICKKVL 188
Db      181 WICKKVL 188

RESULT 2
US-09-811-367B-5
; Sequence 5, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-811-367B-5

Query Match      81.4%; Score 838; DB 9; Length 188;
Best Local Similarity 80.7%; Pred. No. 1.4e-80;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY      1 MADSSIYSTLELPEAPQVQDESRLKAVLHRPHLSRFAMVALGLLTIVILMSLLMYQRI 60
Db      1 MADSSIYSTLELPEAPQVQDESRLKAVLHRPHLSRFAMVALGLLTIVILMSLLMYQRI 60

QY      61 CCGSKDSTCSHCPCPIILWTRNGSHCYFFSMKKDWNSSLKFCADKGSLLTFFPDNQGVK 120
Db      61 CCGSKDSTCSHCPCPIILWTRNGSHCYFFSMKKDWNSSLKFCADKGSLLTFFPDNQGVK 120

QY      121 LFGEYLGQDFYWGILRNIDGWRWEGGPAISL-RILTNSLIQRCGAHNRGLQASSCEVAL 179
Db      121 LFGEYLGQDFYWGILRNIDGWRWEGGPAISL-RILTNSLIQRCGAHNRGLQASSCEVAL 179

QY      181 WICKKVL 187
Db      181 WICKKVL 187

RESULT 3
US-10-207-655-196
; Sequence 196, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 196
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-196

Query Match      55.2%; Score 568.5; DB 14; Length 189;
Best Local Similarity 57.2%; Pred. No. 5.7e-52;
Matches 107; Conservative 25; Mismatches 54; Indels 1; Gaps 1;

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QY      1 MADSSIYSTLELPEAPQVQDESRLKAVLHRPHLSRFAMVALGLLTIVILMSLLMYQRI 60
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QY      61 CCGSKDSTCSHCPCPIILWTRNGSHCYFFSMKKDWNSSLKFCADKGSLLTFFPDNQGVK 120
Db      61 CCGSNYSTCASCPCPDPRWKYGNHCYFFSVEEKDWNSSLEFLCLARDSHLLVITDQEMS 120

QY      121 LFGEYLGQDFYWGILRNIDGWRWEGGPAISL-RILTNSLIQRCGAHNRGLQASSCEVAL 179
Db      121 LLQVFLSEAFWIGLNRNNSGWRWEDGSPNLFNRISSNFVQTCGAINKNGLOASSCEVPL 180

QY      180 QWICKKV 186
Db      181 HWCKKV 187

RESULT 4
US-09-811-367B-1
; Sequence 1, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-367B-1

Query Match      53.3%; Score 548.5; DB 9; Length 189;
Best Local Similarity 55.6%; Pred. No. 7.5e-50;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY      1 MADSSIYSTLELPEAPQVQDESRLKAVLHRPHLSRFAMVALGLLTIVILMSLLMYQRI 60
Db      1 MTDSVIYSMLLELPTAQANDYGPQKSSSSRSCSLVAIALGLLTAVLLSVLLYQWIL 60

QY      61 CCGSKDSTCSHCPCPIILWTRNGSHCYFFSMKKDWNSSLKFCADKGSLLTFFPDNQGVK 120
Db      61 CCGSNYSTCASCPCPDPRWKYGNHCYFFSVEEKDWNSSLEFLCLARDSHLLVITDQEMS 120

QY      121 LFGEYLGQDFYWGILRNIDGWRWEGGPAISL-RILTNSLIQRCGAHNRGLQASSCEVAL 179
Db      121 LLQVFLSEAFWIGLNRNNSGWRWEDGSPNLFNRISSNFVQTCGAINKNGLOASSCEVPL 180

QY      180 QWICKKV 186
Db      181 HGCKKV 187

RESULT 5
US-10-179-528-4
; Sequence 4, Application US/10179528
; Publication No. US20030166136A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive

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OTHER INFORMATION: Incyte ID No. US20030108871A1 516300CD1
US-09-919-039-130

Query Match 17.3%; Score 178.5; DB 10; Length 179;
Best Local Similarity 31.8%; Pred. No. 1.3e-10; Indels 31; Gaps 7;
Matches 54; Conservative 17; Mismatches 68

QY 44 GLLTVILMSLLMYQRIILCCGS-----KDSCTSHCPSPILWTRNGS 84
DB 14 GTLGIIICLSMATLGIILLKNSFTKLSIBPAFTPGPNIELQKSDC--C-SCQEKWVGRC 70
QY 85 HCYYFSMEKKDWNSSLKFCADKGSLLTTPDNQGVKLFGEYLGQDFYWGILRNID---GW 141
DB 71 NCYFISSEQKTWNEGRHLCSQKSLQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128
QY 142 RWEGGPALSRLITN---SLIQRCAIHRNG-LOASSCEVALQWICKVYL 187
DB 129 LWENGSAISOYLFPSFETNTKNCIAYNPNGNALDESCEDKNRYICKQOL 178

RESULT 7
US-10-335-009-10
; Sequence 10, Application US/10335009
; Publication No. US20040001804A1
; GENERAL INFORMATION:
; APPLICANT: Porunelloor, Mathew A.
; TITLE OF INVENTION: LLT USES THEREOF IN IMMUNE SYSTEM MODULATION
; FILE REFERENCE: 11707.02/469687-7
; CURRENT APPLICATION NUMBER: US/10/335,009
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US 09/475,365
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 10
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-009-10

Query Match 17.3%; Score 178.5; DB 15; Length 179;
Best Local Similarity 31.8%; Pred. No. 1.3e-10;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

QY 44 GLLTVILMSLLMYQRIILCCGS-----KDSCTSHCPSPILWTRNGS 84
DB 14 GTLGIIICLSMATLGIILLKNSFTKLSIBPAFTPGPNIELQKSDC--C-SCQEKWVGRC 70
QY 85 HCYYFSMEKKDWNSSLKFCADKGSLLTTPDNQGVKLFGEYLGQDFYWGILRNID---GW 141
DB 71 NCYFISSEQKTWNEGRHLCSQKSLQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128
QY 142 RWEGGPALSRLITN---SLIQRCAIHRNG-LOASSCEVALQWICKVYL 187
DB 129 LWENGSAISOYLFPSFETNTKNCIAYNPNGNALDESCEDKNRYICKQOL 178

RESULT 8
US-09-284-320-86
; Sequence 86, Application US/09284320
; Publication No. US20030092175A1
; GENERAL INFORMATION:
; APPLICANT: Kato, Seishi et al.
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAS
; FILE REFERENCE: GIN-6705CPUS
; CURRENT APPLICATION NUMBER: US/09/284,320
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: JP 8-301429
; PRIOR FILING DATE: 1996-11-13
; PRIOR APPLICATION NUMBER: PCT/JP97/04056
; PRIOR FILING DATE: 1997-11-07

CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/179,528
FILING DATE: 24-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/846,523
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0281 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 505325
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-179-528-4

Query Match 17.7%; Score 182; DB 14; Length 257;
Best Local Similarity 28.7%; Pred. No. 8.3e-11;
Matches 48; Conservative 25; Mismatches 72; Indels 22; Gaps 6;

QY 32 RPHLSRSMYALG---LLTVILMSLLMYQRIILCCGSKDSCTSHCPSPILWTRNGSHCY 87
DB 86 KQNRRLVLCVALSAPVCMVLVALVAVILQBPSC--SPRPFSHV--CFNANWVGQKCY 141
QY 88 YFSMEKKDWNSSLKFCADKGSLLTTPDNQGVKLFGEYLGQDFYWGILRNIDG---WRWE 144
DB 142 YFSDTESDWNSSRHRCHRLGASLATLDTKEEMEFMLQYQREADRWIGLHRAEGDEHTWA 201
QY 145 GGPALSRLITNLSI-----QRCIAHRNGIQAASSCEVALQWICKK 185
DB 202 DGS-----FTNRPVFEIIRGGRCAYLNGDGISSALCHSEKFWVCUR 243

RESULT 6
US-09-919-039-130
; Sequence 130, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 130
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

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; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-284-320-86

Query Match      16.9%; Score 173.5; DB 10; Length 199;
Best Local Similarity 23.8%; Pred. No. 4.8e-10;
Matches 48; Conservative 36; Mismatches 83; Indels 35; Gaps 8;

QY 3 DSSIVSTLELPEAPQVODSRWKLKAVLHRPHLSR-----FAMVALGLLTVILM 51
Db 11 NSSLH-----PESQENDAT-----SPHFSTRHEGSGFQVPLCAVMNVFIIILII 56
QY 52 SL--LMYQRIILCCGSKDSTC---SHCPSPILWTRNGSHCYFFSMKKDNSSLKFCADK 106
Db 57 ALIALSVGQYNCPCQYTFSPDSDSHVSSCSDDWVGQYQKCYFISTVKRSWTSQAQACSEH 116
QY 107 GSHLLTFPDNQGVKLFGEYLQDGYWIGLRNIDG--WRWEGGPALSRLI-LTNSLIQRCG 163
Db 117 GATLAVIDSEKDMNFKRYAGREEHWVGLKEPQHPKWSNGKEFNWNVVTGS--DKCV 174
QY 164 AIHRNGLOASSCEVALQWICKK 185
Db 175 FLKNTVESSMECEKNLYWICNK 196
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RESULT 9
US-10-207-655-182
; Sequence 182, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 182
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-182
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Query Match      16.9%; Score 173.5; DB 14; Length 199;
Best Local Similarity 23.8%; Pred. No. 4.8e-10;
Matches 48; Conservative 36; Mismatches 83; Indels 35; Gaps 8;

QY 3 DSSIVSTLELPEAPQVODSRWKLKAVLHRPHLSR-----FAMVALGLLTVILM 51
Db 11 NSSLH-----PESQENDAT-----SPHFSTRHEGSGFQVPLCAVMNVFIIILII 56
QY 52 SL--LMYQRIILCCGSKDSTC---SHCPSPILWTRNGSHCYFFSMKKDNSSLKFCADK 106
Db 57 ALIALSVGQYNCPCQYTFSPDSDSHVSSCSDDWVGQYQKCYFISTVKRSWTSQAQACSEH 116
QY 107 GSHLLTFPDNQGVKLFGEYLQDGYWIGLRNIDG--WRWEGGPALSRLI-LTNSLIQRCG 163
Db 117 GATLAVIDSEKDMNFKRYAGREEHWVGLKEPQHPKWSNGKEFNWNVVTGS--DKCV 174
QY 164 AIHRNGLOASSCEVALQWICKK 185
Db 175 FLKNTVESSMECEKNLYWICNK 196
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RESULT 10
US-10-179-528-3
; Sequence 3, Application US/10179528
; Publication No. US20030166136A1
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; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Invention: Novel Human C-Type Lectin
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/179,528
; FILING DATE: 24-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,523
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0281 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 291898
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-179-528-3
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Query Match      16.9%; Score 173.5; DB 14; Length 199;
Best Local Similarity 23.8%; Pred. No. 4.8e-10;
Matches 48; Conservative 36; Mismatches 83; Indels 35; Gaps 8;

QY 3 DSSIVSTLELPEAPQVODSRWKLKAVLHRPHLSR-----FAMVALGLLTVILM 51
Db 11 NSSLH-----PESQENDAT-----SPHFSTRHEGSGFQVPLCAVMNVFIIILII 56
QY 52 SL--LMYQRIILCCGSKDSTC---SHCPSPILWTRNGSHCYFFSMKKDNSSLKFCADK 106
Db 57 ALIALSVGQYNCPCQYTFSPDSDSHVSSCSDDWVGQYQKCYFISTVKRSWTSQAQACSEH 116
QY 107 GSHLLTFPDNQGVKLFGEYLQDGYWIGLRNIDG--WRWEGGPALSRLI-LTNSLIQRCG 163
Db 117 GATLAVIDSEKDMNFKRYAGREEHWVGLKEPQHPKWSNGKEFNWNVVTGS--DKCV 174
QY 164 AIHRNGLOASSCEVALQWICKK 185
Db 175 FLKNTVESSMECEKNLYWICNK 196
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RESULT 11
US-10-379-127-26
; Sequence 26, Application US/10379127
; Publication No. US20040005592A1
; GENERAL INFORMATION:
; APPLICANT: Emtage, Peter C.R.
; APPLICANT: Drmanac, Radoje
; APPLICANT: Goodrich, Ryle
```


QY 137 NIDG-WRGGGPPALSRLILNLSLQRCGA-----IHRNG-----LQAS-----SC 175
DB 477 GTEGSRWTDGTPF-----NAAQNGFWKXQSDNWRHKNQGTEDCVQIQOKWDMTC 529
QY 176 EVALOWICKK 185
DB 530 DTPYQWVCKK 539

RESULT 14

US-10-072-012-160
; Sequence 160, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Bsha
; APPLICANT: Padigar, Muraidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 160
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-072-012-160

Query Match 16.5%; Score 170; DB 12; Length 549;
Best Local Similarity 30.0%; Pred. No. 3.9e-09;

Matches 39; Conservative 17; Mismatches 44; Indels 30; Gaps 6;
QY 79 WTRNGSHCYFSEMEKOWNSSLKFCADKSHLLTFPDNGVKLFGEYLGQDFWIGL--R 136
DB 420 WKFNGLSYFSSVKKSWEAEQFCVSOQAHLASVASKEEQAFLEFTSKVYVWIGLTD 479
QY 137 NIDG-WRGGGPPALSRLILNLSLQRCGA-----IHRNG-----LQAS-----SC 175
DB 480 GTEGSRWTDGTPF-----NAAQNGFWKXQSDNWRHKNQGTEDCVQIQOKWDMTC 532
QY 176 EVALOWICKK 185
DB 533 DTPYQWVCKK 542

RESULT 15

US-10-179-528-7
; Sequence 7, Application US/10179528
; Publication No. US20030166136A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/179,528
; FILING DATE: 24-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,523
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0281 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 584907
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-179-528-7

Query Match 16.3%; Score 168; DB 14; Length 199;
Best Local Similarity 24.1%; Pred. No. 1.9e-09;
Matches 39; Conservative 34; Mismatches 67; Indels 22; Gaps 5;
QY 38 FAWVALGLLTWILMSLL-----MYQRILCCGSKDSTCHSCFPIILWRNHSHC 86
DB 43 WAVLIVLITSLIALALNKGKNCPLFEKL-----ESSDHHVATCKNWSYKRTC 96
QY 87 YFSEMEKOWNSSLKFCADKSHLLTFPDNGVKLFGEYLGQDFWIGLNR--IDGWRWE 144

Db 97 YFESTTTKSWALQORSCSEDAATLAVIDSEKDMTFLKRYSGELEHHWIGLKNEANQTKWA 156

Qy 145 GGPAL-SLRILTNSLIQRCGAIHRNGLQASSCEVALQWICKK 185

Db 157 NGKEFNSWFNLTGS--GRCVSVNHKNVTAVDCEANFHWVCSK 196

Search completed: August 10, 2004, 16:32:37
Job time : 41.2619 secs

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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:13:57 ; Search time 14.6407 Seconds
(without alignments)
662.924 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029

Sequence: 1 MADSSTSTLELPEAPQVQD.....GLQASCEVALQWICKKVLV 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	838	81.4	188	3	US-08-722-126A-5
2	838	81.4	188	5	PCT-US95-04258-5
3	551	53.5	114	3	US-08-722-126A-6
4	551	53.5	114	5	PCT-US95-04258-6
5	267	25.9	76	4	US-09-531-056A-23
6	178.5	17.3	179	1	US-08-690-095-9
7	178.5	17.3	179	2	US-08-650-578-2
8	178.5	17.3	179	2	US-08-688-342-3
9	178.5	17.3	179	2	US-09-113-788-3
10	178.5	17.3	179	3	US-09-113-789-9
11	173.5	16.9	199	5	PCT-US93-10418-2
12	168	16.3	199	5	PCT-US93-10418-4
13	164.5	16.0	225	2	US-08-738-462-2
14	164.5	16.0	225	5	PCT-US94-07587-2
15	163.5	15.9	191	4	US-09-531-056A-6
16	160.5	15.6	231	1	US-08-690-095-6
17	160.5	15.6	231	3	US-09-113-789-6
18	160.5	15.6	231	3	US-08-543-246B-6
19	160.5	15.6	231	3	US-08-543-246B-23
20	154	15.0	190	4	US-09-127-946-14
21	153	14.9	316	3	US-09-111-470-4
22	152.5	14.8	1479	3	US-08-840-062-2
23	152	14.8	122	3	US-08-722-126A-9
24	152	14.8	122	5	PCT-US95-04258-9
25	152	14.8	215	1	US-08-690-095-7
26	152	14.8	215	3	US-09-113-789-7
27	152	14.8	215	3	US-08-543-246B-16

28 152 14.8 215 3 US-08-543-246B-22
29 151 14.7 233 1 US-08-690-095-8
30 151 14.7 233 3 US-09-113-789-8
31 151 14.7 233 3 US-08-543-246B-2
32 151 14.7 233 3 US-08-543-246B-21
33 151 14.7 1487 3 US-08-840-062-7
34 150.5 14.6 115 3 US-08-722-126A-8
35 150.5 14.6 115 5 PCT-US95-04258-8
36 150 14.6 328 4 US-09-531-056A-13
37 149 14.5 404 4 US-09-517-605-2
38 148 14.4 194 4 US-09-531-056A-2
39 147.5 14.3 273 3 US-09-111-470-10
40 147.5 14.3 292 2 US-08-688-342-4
41 147.5 14.3 292 2 US-09-113-788-4
42 146 14.2 135 3 US-08-543-246B-19
43 145 14.1 173 4 US-09-531-056A-4
44 144 14.0 216 3 US-08-543-246B-9
45 144 14.0 216 3 US-08-543-246B-24

ALIGNMENTS

RESULT 1
US-08-722-126A-5
; Sequence 5, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-722-126A-5

Query Match 81.4%; Score 838; DB 3; Length 188;
Best Local Similarity 80.7%; Pred. No. 1.8e-86;

	Matches	151;	Conservative	15;	Mismatches	21;	Indels	0;	Gaps	0;
Qy	1	MADSSIIYSTLELPEAPQVQDES	RWKLKAVLRPHLSRFAMVALGLT	VILMSLLMYORIL	60					
Dd	1	MADNSIYSTLELPAAPRVQDSDR	RWKVKAVLRHPCVSYLVMVALGLT	VILMSLLLYQRTL	60					
Qy	61	CCGSKDSTCSHCPSCPILLTRNG	SCHCYFFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK	120						
Dd	61	CCGSKGPMCSQCSCPMLWRNG	SCHCYFFSMEKRDNWSLKFCDKGSHELLTFPDNQGVN	120						
Qy	121	LFGYLGDFWIGWLGRINDGWREGG	PALSURLITNSLIORCGATHRNGLQASSCEVALQ	180						
Dd	121	LFQEYVEDFWIGLGRIDGHWEDG	FALSSLISNVVQXCGTHRCGLFASCEVALQ	180						
Qy	181	WICKKVL	187							
Dd	181	WICEKVL	187							

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1  RESULT 2
2  PCT-US95-04258-5
3  Sequence 5, Application PC/TUS9504258
4  GENERAL INFORMATION:
5  APPLICANT:
6  TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
7  TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
8  NUMBER OF SEQUENCES: 10
9  CORRESPONDENCE ADDRESS:
10 ADDRESSEE: BROWDY AND NEIMARK
11 STREET: 419 Seventh Street, N.W., Suite 300
12 CITY: Washington
13 STATE: D.C.
14 COUNTRY: USA
15 ZIP: 20004
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: PCT/US95/04258
23 FILING DATE: 06-APR-1995
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: IL 109257
26 FILING DATE: 08-APR-1994
27 ATTORNEY/AGENT INFORMATION:
28 NAME: BROWDY, Roger L.
29 REGISTRATION NUMBER: 25,618
30 REFERENCE/DOCKET NUMBER: PCHT=1 PCT
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: 202-628-5197
33 TELEFAX: 202-737-3528
34 TELEX: 248633
35 INFORMATION FOR SEQ ID NO: 5:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 188 amino acids
38 TYPE: amino acid
39 TOPOLOGY: linear
40 MOLECULE TYPE: protein
41 PCT-US95-04258-5

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[illegible]

RESULT 4
PCT-US95-04258-6

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; Sequence 6, Application PC/TUS9504258
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04258-6

Query Match 53.5%; Score 551; DB 5; Length 114;
Best Local Similarity 84.1%; Pred. No. 2e-54; Indels 0; Gaps 0;
Matches 95; Conservative 9; Mismatches 9;

QY 75 CPILWTRNGSHCYFYSMEKDWNSLKFCDKSGHLLTFPDNQGKLFGEYLGQDFYWG 134
Db 1 CPNLWNRNGSHCYFYSMEKDWNSLKFCDKSGHLLTFPDNQGKLFGEYVGEDFYWG 60

QY 135 LRNIDGWRWEGGPAISLRILTNLSLIQRCGAHNRGLQASCEVALQWICKVL 187
Db 61 LRIDGWRWEDGPAISLSILNSVYQCGTIHROGLHASCEVALQWICKVL 113

RESULT 5
US-09-531-056A-23
; Sequence 23, Application US/09531056A
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531.056A
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-531-056A-23
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Query Match 25.9%; Score 267; DB 4; Length 76;
Best Local Similarity 59.5%; Pred. No. 1.2e-22;
Matches 44; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 73 PSCPILWTRNGSHCYFYSMEKDWNSLKFCDKSGHLLTFPDNQGKLFGEYLGQDFYWG 132
Db 1 PSCPDRMKYGNHCYFYSVEEKDWNSLKFCLARDSHLLVITDQEMSLIQVFLSEAFW 60

QY 133 IGLRNIDGWRWEGG 146
Db 61 IGLRNKSGWRWEDG 74

RESULT 6
US-08-690-095-9
; Sequence 9, Application US/08690095
; Patent No. 5792648
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,095
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0110 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098617
US-08-690-095-9

Query Match 17.3%; Score 178.5; DB 1; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.5e-12;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

QY 44 GLTIVILMSLLMYQRIILCCGS-----KSTCSHCSPCPILWTRNGS 84
Db 14 GTLGIICLSMATLIGILLKNSFTKLSTIEPAFTPGPNIELQKSDC--C-SCQKQWVGRC 70

QY 85 HCYFYSMEKDWNSLKFCDKSGHLLTFPDNQGKLFGEYLGQDFYWGIRNID---GW 141
Db 71 NCYFISSEQKTWNEASHLCASQKSSLLQLQNTDELDFMSS--SQCFYWGILSYSEHTAW 128

QY 142 RWEGGPAISLRILTN---SLIQRCGAHNRNG-LQASCEVALQWICKVL 187
Db 129 LWENGSAISOYLFPSPEFTFNKCIAYNPNGNALDESCEDKNRYICKQQL 178
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RESULT 7

US-08-650-578-2
; Sequence 2, Application US/08650578
; Patent No. 5811284
; GENERAL INFORMATION:
; APPLICANT: Chang, Chiwen
; APPLICANT: Aramburu Beltran, Jose
; APPLICANT: Lopez-Botet, Miguel
; APPLICANT: Phillips Jr., Joseph H.
; APPLICANT: Lanier, Lewis L.
; TITLE OF INVENTION: Purified Mammalian NK Antigens and
; TITLE OF INVENTION: Related Reagents
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650,578
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,339
; FILING DATE: 29-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-650-578-2

Query Match 17.3%; Score 178.5; DB 2; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.5e-12;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

QY 44 GLLTVILMSLLMYQRIKCGS-----KDTSCSHCPSCPIILWTRNGS 84
DB 14 GTLGICLSLMTATLIGLLKNSFTKLSIEPAFTPGNIELQKSDC--C-SCQEKWVGRC 70
QY 85 HCYFSEKMDKWNSSLKFCADKGSLLTFFPDNQGVKLFGEYLGQDFYWGILRNID---GW 141
DB 71 NCYFISSEQKTWNSRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128
QY 142 RWEGGPALSLRLTN---SLIQRCGAIHRNG-LQASCEVALQWICKVYL 187
DB 129 LWENGSAISQVLFPSFETFKNCIAYPNNGNALDESCEDCKNRYICKQOL 178

RESULT 8

US-08-688-342-3
; Sequence 3, Application US/08688342
; Patent No. 5871964
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/688,342
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0095-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098616
; US-08-688-342-3

Query Match 17.3%; Score 178.5; DB 2; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.5e-12;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

QY 44 GLLTVILMSLLMYQRIKCGS-----KDTSCSHCPSCPIILWTRNGS 84
DB 14 GTLGICLSLMTATLIGLLKNSFTKLSIEPAFTPGNIELQKSDC--C-SCQEKWVGRC 70
QY 85 HCYFSEKMDKWNSSLKFCADKGSLLTFFPDNQGVKLFGEYLGQDFYWGILRNID---GW 141
DB 71 NCYFISSEQKTWNSRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128
QY 142 RWEGGPALSLRLTN---SLIQRCGAIHRNG-LQASCEVALQWICKVYL 187
DB 129 LWENGSAISQVLFPSFETFKNCIAYPNNGNALDESCEDCKNRYICKQOL 178

RESULT 9

US-09-113-788-3
; Sequence 3, Application US/09113788
; Patent No. 5969104
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:


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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,788
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/688,342
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098616
; US-09-113-788-3

Query Match 17.3%; Score 178.5; DB 2; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.5e-12;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

Qy 44 GLLTVILMSLLMYQRIILCCGS-----KSTCSHCPCSPILWTRNGS 84
Db 14 GTLGIIICLSMATLIGILLKNSFTKLSIEPAFTPGPNIELQKSDC--C-SCQEKWVGRC 70

Qy 85 HCYFYSMEKKDWNSSLKFCADKGSLLHTFFPNQGVKLFGEYLGQDFYWGIRNID---GW 141
Db 71 NCYFISSEQKTWNSRHLCASQKSLQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128

Qy 142 RWEGGPALSRLITN---SLIQRCGAHRNG-LQASCEVALQWICKKVL 187
Db 129 LWENGSAISQVLFPSFETFTKNCIAYNPNGNALDESCEDKNRYICKQOL 178

RESULT 10
US-09-113-789-9
; Sequence 9, Application US/09113789
; Patent No. 6034219
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,789
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/690,095

```

```

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0110 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098617
; US-09-113-789-9

Query Match 17.3%; Score 178.5; DB 3; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.5e-12;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

Qy 44 GLLTVILMSLLMYQRIILCCGS-----KSTCSHCPCSPILWTRNGS 84
Db 14 GTLGIIICLSMATLIGILLKNSFTKLSIEPAFTPGPNIELQKSDC--C-SCQEKWVGRC 70

Qy 85 HCYFYSMEKKDWNSSLKFCADKGSLLHTFFPNQGVKLFGEYLGQDFYWGIRNID---GW 141
Db 71 NCYFISSEQKTWNSRHLCASQKSLQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128

Qy 142 RWEGGPALSRLITN---SLIQRCGAHRNG-LQASCEVALQWICKKVL 187
Db 129 LWENGSAISQVLFPSFETFTKNCIAYNPNGNALDESCEDKNRYICKQOL 178

RESULT 11
PCT-US93-10418-2
; Sequence 2, Application PC/TUS9310418
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Steven F.
; APPLICANT: Hjerild, Kathryn A.
; TITLE OF INVENTION: Activation Antigen CD69
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10418
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2610-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```



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RESULT 14
PCT-US94-07587-2
; Sequence 2, Application PC/TUS9407587
; GENERAL INFORMATION:
; APPLICANT: Schering Corp.
; TITLE OF INVENTION: PURIFIED MAMMALIAN NK ANTIGENS AND
; TITLE OF INVENTION: RELATED REAGENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Schering Corp.
; STREET: One Giralda Farms
; CITY: Madison
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07940
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07587
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lund, Paul G.
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: DX0397K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-822-7255
; TELEFAX: 201-822-7039
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07587-2

Query Match 16.0%; Score 164.5; DB 5; Length 225;
Best Local Similarity 27.4%; Pred. No. 1.8e-10;
Matches 60; Conservative 32; Mismatches 90; Indels 37; Gaps 10;

Qy 1 MADSIYSTLELP--EAPQ-----VDSRWKLVKAVLHRPHLSRFAMVALGL--- 45
Db 1 MDQQAIAELNLPTDGPSESSSLPRDVCQSPWHQFAL----KLSAGIILLVLVVT 56

Qy 46 -LTVILMSLLMYQRIILCG-----SKDSTCSH--CPSCPILWTRNGSHCYFYSMEKKDWN 97
Db 57 GLSVSVTSLIQKSSIEKCSVDIQSRNKTTPRGILNCPYVQQQLREKCLLFSTVNPWN 116

Qy 98 SSLKFCADRGSHLTFPPDNQGVKLFGBYLQD---FYWIGLR---NIDGWRWEGGPALS- 150
Db 117 NSLADCSTKESLLLRDKDEL-IHTQNLIRDKAILEWIGLNFSLSEKNKWKINGSFLNS 175

Qy 151 --LRILTNSLIQRCGAHRNGLQASSCEVALQWICKVL 187
Db 176 NDLEIRGDAKENSCISISQTSVYSEYCSYTCIRWICQKEL 214

RESULT 15
US-09-531-056A-6
; Sequence 6, Application US/09531056A
; Patent No. 6455683
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI
; FILE OF INVENTION: PROTEINS
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531,056A
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent version 3.0
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; SEQ ID NO 6
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-531-056A-6

Query Match 15.9%; Score 163.5; DB 4; Length 191;
Best Local Similarity 25.3%; Pred. No. 1.9e-10;
Matches 50; Conservative 21; Mismatches 78; Indels 49; Gaps 7;

Qy 11 ELPEAPQVQDESRLKLVKAVLHRPHLSRFAMVALGLTIVL--LMSLLMYQRIILCG----- 63
Db 15 ELPANPCLHSKHSIKA-----TLIWLRLFLINFLTIIVCGMVAAL 56

Qy 64 -SKDSTCSHCP-----CPILWTRNGSHCYFYSMEKKDWNSSILKFCADRGSHLTFPPDN 116
Db 57 SAIRANCHQEPSVCLQAACPESWIGFQKCFYFSDTKNTWTSQRFCDSDADLAQVESF 116

Qy 117 QGVKLFGEYLGQDFYWIGLGNIDG--WRWEGG-----FALSRLITLNSLIQRCGAHR 167
Db 117 QELNFLRYKGPSDHWIGLSRREGQPKWKWINGTWTQFPILG-----AGECAYLND 168

Qy 168 NGLQASSCEVALQWICKK 185
Db 169 KGASSARHYTERKWICKS 186

Search completed: August 10, 2004, 16:20:31
Job time : 14.6407 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2004, 16:12:27 ; Search time 11.9788 Seconds
(without alignments)
1509.673 Million cell updates/sec

Title: US-09-811-367B-5
Perfect score: 1036
Sequence: 1 MADNSIYSTLELPAPRVQD.....GLHASCEVALQWICEKVLP 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: Piri.*
2: Piri2.*
3: Piri3.*
4: Piri4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	2 I59421	mast cell function
2	184.5	17.8	199	2 JH0822	lymphocyte early a
3	184	17.8	257	2 I50146	gene 17.5 protein
4	172.5	16.7	227	2 A46467	natural killer cel
5	169.5	16.4	225	2 I38700	hNKR-P1a protein -
6	167	16.1	223	2 B46467	NKR-P1 protein hom
7	165.5	16.0	301	1 LNRT2	hepatic lectin 2 -
8	162.5	15.7	170	2 T28140	natural killer cell
9	159.5	15.4	220	2 C46467	NKR-P1 protein hom
10	159.5	15.4	223	2 A35917	NK-cell receptor P
11	159.5	15.4	301	2 S13165	asialoglycoprotein
12	158	15.3	156	2 T28141	C type lectin, B 1
13	158	15.3	1487	2 S48719	phospholipase-A(2)
14	157	15.2	216	2 P70375	natural killer cel
15	156	15.1	284	2 S29855	asialoglycoprotein
16	154.5	14.9	304	2 JX0209	lectin, galactose/
17	153.5	14.8	404	2 A46274	HIV gp120-binding
18	153.5	14.8	742	2 J75595	scavenger receptor
19	148.5	14.3	306	2 A42230	lectin M-ASGP-BP p
20	148	14.3	237	2 J76088	type II lectin-like
21	146	14.1	146	2 J7135	agglutinin beta
22	142.5	13.8	233	2 P70372	natural killer cel
23	142.5	13.8	359	2 A43532	B-cell surface ant
24	141.5	13.7	1326	2 A36395	secretory phosphol
25	141.5	13.7	1465	2 A56395	secretory phosphol
26	140.5	13.6	311	1 LNHU2A	asialoglycoprotein
27	139	13.4	240	2 I54524	natural killer cel
28	139	13.4	284	1 LNRTL	hepatic lectin - r
29	137	13.2	167	1 WNVZF2	hepatic lectin hom

hepatic lectin - c
natural killer cel
agglutinin alpha cha
mannose receptor,
hepatic lectin H1
versican precursor
phospholipase A2 r
IgE Fc receptor, l
Kupffer cell recep
versican precursor
versican precursor
ly-49G.2 antigen -
versican precursor
IgE Fc receptor II
coagulation factor
receptor DEC-205 -

ALIGNMENTS

RESULT 1

I59421
mast cell function associated antigen - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I59421
R:Guthmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A:Title: A secretion inhibitory signal transduction molecule on mast cells is another C
A:Reference number: I59421; MUID:96016176; PMID:7568140
A:Accession: I59421
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-188 <RES>
A:Cross-references: EMBL:X79812; NID:g1020141; PIDN:CAA56208.1; PID:g1020142
C:Genetics:
A:Gene: mafa

Query Match 100.0%; Score 1036; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 3.2e-90;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MADNSIYSTLELPAPRVQDSSRWKAVLRPCVSYLVWVAGLLTVILMSLLLYORTL	60
Db	1	MADNSIYSTLELPAPRVQDSSRWKAVLRPCVSYLVWVAGLLTVILMSLLLYORTL	60
Qy	61	CCGSKGFMCQCRCPNLWRNGSHCYFFSMKRDWNSLKFCAKDGSHLITFPDNGVN	120
Db	61	CCGSKGFMCQCRCPNLWRNGSHCYFFSMKRDWNSLKFCAKDGSHLITFPDNGVN	120
Qy	121	LFQYVGEDFYWIGLRIDGWRWEDGPAISLSILNSVQKCGTHRCGLHASCEVALQ	180
Db	121	LFQYVGEDFYWIGLRIDGWRWEDGPAISLSILNSVQKCGTHRCGLHASCEVALQ	180
Qy	181	WICEKVLP 188	
Db	181	WICEKVLP 188	

RESULT 2

JH0822
lymphocyte early activation antigen AIM/CD69 - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 08-Oct-1999
C:Accession: JH0822; I56167; S60753
R:Lopez-Cabrera, M.; Santis, A.G.; Fernandez-Ruiz, E.; Blacher, R.; Esch, F.; Sanchez-M
J. Exp. Med. 178, 537-547, 1993
A:Title: Molecular cloning, expression, and chromosomal localization of the human earli
mitting receptors.
A:Reference number: JH0822; MUID:93340630; PMID:8340758
A:Accession: JH0822
A:Molecule type: mRNA

A;Residues: 1-199 <LQP>
A;Cross-references: GB:Z22576; NID:9397938; PIDN:CAA80298.1; PID:9397939
A;Note: the authors translated the codon CAA for residue 110 as Glu
R;Hamann, J.; Fiebig, H.; Strauss, M.
J. Immunol. 150, 4920-4927, 1993
A;Title: Expression cloning of the early activation antigen CD69, a type II integral membrane protein
A;Reference number: I56167; MUID:93267093; PMID:8496594
A;Accession: I56167
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-199 <RES>
A;Cross-references: GB:L07555; NID:9291897; PIDN:AAB46359.1; PID:9291898
R;Santis, A.G.; Lopez-Cabrera, M.; Hamann, J.; Strauss, M.; Sanchez-Madrid, F.
Eur. J. Immunol. 24, 1692-1697, 1994
A;Title: Structure of the gene coding for the human early lymphocyte activation antigen CD69.
A;Reference number: S60753; MUID:94298875; PMID:8026529
A;Accession: S60753
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-199 <SAN>
A;Cross-references: EMBL:Z30426; NID:9525242; PIDN:CAA83017.1; PID:9558352
C;Comment: This protein is the earliest inducible cell surface glycoprotein expressed in T cells.
A;Genetics: GDB:CD69
A;Cross-references: GDB:132925; OMIM:107273
A;Map position: 12p13-12p12
C;Superfamily: C-type lectin homology
C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F;39-64/Domain: transmembrane #status predicted <TM>
F;85-194/Domain: C-type lectin homology <LCH>
F;18,30/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;31/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted
F;166/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 17.8%; Score 184.5; DB 2; Length 199;
Best Local Similarity 26.3%; Pred. No. 4.7e-10;
Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;
35 VSILVVALGLTTLVILSLLYQRTLCCKSGKFCMC---SQSCRCPLNWMNGSHCHYFYSM 91
45 VMNVVFIILLIALISVGQV---CQGYTFSPSHVSSCSSEDWVGQKCYFIST 101
92 EKRDWNSLKFCADKSGHLLTPDNGQVNLFOYVGEDFYWIGLRDIDG---WRWEDGPAL 149
102 VKRSWTSQNAACSEHGATLAVIDSEKDMFLKRYAGREHWGLKKEPCHPWKNGKEF 161
150 SLISLSNSVQKCGTHRCGLHASSCEVALQWICEK 185
162 N-NWPNVTGSDKCVFLKNTVSSMECEKNLYWICNK 196
Query Match 17.8%; Score 184; DB 2; Length 257;
Best Local Similarity 28.6%; Pred. No. 6.8e-10;
Matches 46; Conservative 23; Mismatches 66; Indels 26; Gaps 6;
150146
gene 17.5 protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I50146
R;Bernot, A.; Zoorob, R.; Auffray, C.
Immunogenetics 39, 221-229, 1994
A;Title: Linkage of a new member of the lectin supergene family to the chicken Mhc genes
A;Reference number: I50146; MUID:94164691; PMID:8119728
A;Accession: I50146
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-257 <BER>
A;Cross-references: GB:M88072; NID:9505324; PIDN:AAA48558.1; PID:9505325
C;Superfamily: C-type lectin homology
F;129-241/Domain: C-type lectin homology <LCH>
Query Match 17.8%; Score 184; DB 2; Length 257;
Best Local Similarity 28.6%; Pred. No. 6.8e-10;
Matches 46; Conservative 23; Mismatches 66; Indels 26; Gaps 6;

33 PCVSYLVVALGLTTLVILSLLYQRTLCCKSGKFCMCQSCRCPLNWMNGSHCHYFYSME 92
101 PC-----MLVLAVAVIL-----ORPSCSPRPFP-----SHVCPNANWVGQKCYFIST 146
93 KRDWNSLKFCADKSGHLLTPDNGQVNLFOYVGEDFYWIGLRDIDG---WRWEDGPAL 149
147 ESDWNSRREHCHRLGASLATLDTKEEMEFMLQYQRPADRWIGLHRAEGDEHTWADGSF 206
150 SLISLSNSVQKCGTHRCGLHASSCEVALQWICEK 185
207 T-----NRPFVELRGCGRCAYLNGDGISSALCHSEKFWVCSSR 243
RESULT 4
A;Accession: A46467
A;Title: natural killer cell receptor P1 - mouse
N;Alternate names: NKR-P1 protein
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 19-Feb-1999 #text_change 05-May-2000
C;Accession: A46467; A46502; A46456
R;Giorda, R.; Trucco, M.
J. Immunol. 147, 1701-1708, 1991
A;Title: A family of genes selectively coexpressed in adherent lymphokine-activated killer cells
A;Reference number: A46467; MUID:91349596; PMID:1880421
A;Accession: A46467
A;Molecule type: mRNA
A;Residues: 'MLLCT', 1-227 <GIO>
A;Cross-references: GB:M77676; NID:9200058
A;Experimental source: A-LAK cells, C57BL
A;Note: sequence extracted from NCI backbone (NCBIN:52378, NCBIP:52379); the sequence
R;Giorda, R.; Weisberg, E.P.; Ip, T.K.; Trucco, M.
J. Immunol. 149, 1957-1963, 1992
A;Title: Genomic structure and strain-specific expression of the natural killer cell receptor gene
A;Reference number: A46502; MUID:92388663; PMID:1517565
A;Accession: A46502
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109, 'H', 111-181, 'D', 183-227 <GI2>
A;Cross-references: GB:X64716; NID:953395; PIDN:CAA45971.1; PID:9817989
A;Experimental source: BALB/c 3T3 fibroblastoid cell line
A;Note: sequence extracted from NCI backbone (NCBIN:113037, NCBIN:113063, NCBIN:113072)
R;Yokoyama, W.M.; Ryan, J.C.; Hunter, J.J.; Smith, H.R.; Stark, M.; Seaman, W.E.
J. Immunol. 147, 3229-3236, 1991
A;Title: cDNA cloning of mouse NKR-P1 and genetic linkage with LY-49. Identification of
A;Reference number: A46456; MUID:92013158; PMID:1680927
A;Accession: A46456
A;Molecule type: mRNA
A;Residues: 1-38, 'L', 40-227 <YOK>
A;Cross-references: GB:M77753; NID:9198569; PIDN:AAA39366.1; PID:9198570
A;Note: sequence extracted from NCI backbone (NCBIN:60429, NCBIP:60431)
C;Superfamily: natural killer cell receptor P1; C-type lectin homology
F;94-210/Domain: C-type lectin homology <LCH>
Query Match 16.7%; Score 172.5; DB 2; Length 227;
Best Local Similarity 24.4%; Pred. No. 7.2e-09;
Matches 53; Conservative 35; Mismatches 86; Indels 43; Gaps 8;
6 IYSTILELPAAPRVQDDSRWKV-----KAVLHRRPCVSYLVVALGLTTLVILSLL 54
6 VYFGLKPTPTGAWHESPPSLPPDACCRCPRSRSAKLSCAGLILV-----VTILGMSVL 61
55 -----LYQRTLCCKSGKFCMCQSCRCPLNWMNGSHCHYFYSMEKRDWNS 99
62 VRVLIQKPSIEKCVLIQENL---NKTTCGAKLECPQDWLSHRDKCFHVQSVNTWEEG 118
100 LKFCADKSGHLLTPDNGQVNLFOYVGEDF--TWIGLR-----DIDGWEDGPALS--- 150
119 LVDGCGKATLMLIQDQELRFLDLSIKEKYNSEFWIGLRYTLPDWN--NKLINGSTLNSDV 177
151 LSILSNSVQKCGTHRCGLHASSCEVALQWICEKVL 187
178 LKITGDTENDSCAAISGDKVTTFESCSNDRWICQEL 214

```
RESULT 5
I38700
hNKR-P1a protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C;Accession: I38700
R;Janier, L.L.; Chang, C.; Phillips, J.H.
J. Immunol. 153, 2417-2428, 1994
A;Title: Human NKR-P1A: A disulfide-linked homodimer of the C-type lectin superfamily ex
A;Reference number: I38700; MUID:94358407; PMID:8077657
A;Accession: I38700
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-225 <RES>
A;Cross-references: EMBL:U11276; NID:9538270; PIDN:AAA21605.1; PID:9544496
C;Superfamily: natural killer cell receptor P1; C-type lectin homology
F;94-210/Domain: C-type lectin homology <LCH>

Query Match 16.4%; Score 169.5; DB 2; Length 225;
Best Local Similarity 26.1%; Pred. No. 1.4e-08;
Matches 59; Conservative 32; Mismatches 84; Indels 51; Gaps 11;

QY 1 MADNSIYSTLELP-----AAPR-VQDDSRKVKAVLHRC--VSYLVMVALGLL 46
Db 1 MDQQAIIAELMLPTDGPSSPSLPRDVCQGSFWH-QFALKUSCAGIILLVLVVTG-L 58
QY 47 TVILMSLLLYQRTLCGSGKGMFCQCS-----SIEKSVDIQQRNKTTERPGLLNCPIYQQLREKCLLF 89
Db 59 SVSVTSII-QKS-----SIEKSVDIQQRNKTTERPGLLNCPIYQQLREKCLLF 108
QY 90 SMEKRDVNSLKFADKGGSHLLTFPDNQGNLFEYVGED--FWIGLR----DIDGWRWE 144
Db 109 SHTVNPWNLSADGSTRESSLLIRDKDELHTQNLIRDKAILFWMIGLNFSLSEKNKWI 168
QY 145 DGPALS---LSILNSVVQKGTTHRCGLHASSCEVALQWICEKVL 187
Db 169 NGSFLNSDLIRGDAKENSICISQTSVSYSEYCSIEIRWICQKEL 214

RESULT 6
B46467
NKR-P1 protein homolog - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
C;Accession: B46467
R;Giorda, R.; Trucco, M.
J. Immunol. 147, 1701-1708, 1991
A;Title: A family of genes selectively coexpressed in adherent lymphokine-activated kill
A;Reference number: A46467; MUID:91349596; PMID:1880421
A;Accession: B46467
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-223 <GIO>
A;Cross-references: GB:M77677; NID:9200060; PIDN:AAA39823.1; PID:9200061
A;Experimental source: NK cells, C57BL/7B
A;Note: sequence extracted from NCBI backbone (NCBIN:52380, NCBI:P:52381)
C;Superfamily: natural killer cell receptor P1; C-type lectin homology
C;Keywords: transmembrane protein
F;94-210/Domain: C-type lectin homology <LCH>

Query Match 16.1%; Score 167; DB 2; Length 223;
Best Local Similarity 23.3%; Pred. No. 2.3e-08;
Matches 50; Conservative 34; Mismatches 91; Indels 40; Gaps 8;

QY 6 IYSTLELPAAPRVQDSS-----RKVKAVLHRCPCVSY-----LVMVALGLL 46
Db 7 VYADINLARIQEPKHDSPPSLSPDTCRCPRW-----HRLALKFCAGIILLVLVVTG 60
QY 47 TVILMSLLLYQRTLCG-----SKGFMGSCQSRCPNLWNRNGSHCYFYSMEKRDVNSLSLK 101
Db 61 VLIVSVQKSSVQKICADVQENRTHTDCSVNLECPQDMLSHRDKCFRVFQVSNTWEEGQA 120
```

```
QY 102 FCADKGGSHLLTFPDNQGNLFEYVGEDF--YWIGLR----DIDGWRWEDGPALS---LS 152
Db 121 DCGRKGATLLLIQDBELRPLLSIRKYNFGLRFTLPDMN-KWINGTTFNSDVLK 179
QY 153 ILNSVVQKGTTHRCGLHASSCEVALQWICEKVL 187
Db 180 ITGDTENGSCASISGDKVTSESCTDNRWICQKEL 214

RESULT 7
LNRT2
hepatic lectin 2 - rat
N;Alternate names: asialoglycoprotein receptor RHL-2/3 (ASGP-R2/3)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1988 #sequence_revision 09-Apr-1998 #text_change 22-Jun-1999
C;Accession: B28462; A28462; A31601; A26888; A25417
R;Halberg, D.F.; Wager, R.E.; Farrell, D.C.; Hildreth IV, J.; Quesenberry, M.S.; Loeb, J.
J. Biol. Chem. 262, 9828-9838, 1987
A;Title: Major and minor forms of the rat liver asialoglycoprotein receptor are indepen
A;Reference number: A28462; MUID:87250656; PMID:3597443
A;Accession: B28462
A;Molecule type: mRNA
A;Residues: 1-301 <HAL>
A;Cross-references: GB:J02762; NID:g205162; PIDN:AAA41522.1; PID:g205163
A;Accession: A28462
A;Molecule type: protein
A;Residues: 88-96; 'X', 98-118; 'X', 120; 129-158; 177-182; 'X', 184; 'X', 186-189; 192-290; 'C', 29
R;Sanford, J.P.; Elliott, R.W.; Doyle, D.
DNA 7, 721-728, 1988
A;Title: Asialoglycoprotein receptor genes are linked on chromosome 11 in the mouse.
A;Reference number: A31601; MUID:89170119; PMID:3234178
A;Accession: A31601
A;Molecule type: mRNA
A;Residues: 1-301 <SAN>
A;Cross-references: GB:X07636; NID:g57066; PIDN:CAA30476.1; PID:g57067
R;McPhaul, M.; Berg, P.
Mol. Cell. Biol. 7, 1841-1847, 1987
A;Title: Identification and characterization of cDNA clones encoding two homologous pro
A;Reference number: A26888; MUID:87257885; PMID:3600647
A;Accession: A26888
A;Molecule type: mRNA
A;Residues: 1-152; 'A', 154-201; 'I', 203-259; 'C', 261-301 <MCP>
A;Cross-references: GB:M16347; NID:g206648; PIDN:AAA42038.1; PID:g206649
A;Note: the authors translated the codon GCA for residue 153 as Arg and ATT for residue
R;Drickamer, K.; Mamou, J.F.; Binns, G.; Leung, J.O.
J. Biol. Chem. 259, 770-778, 1984
A;Title: Primary structure of the rat liver asialoglycoprotein receptor: structural evi
A;Reference number: A25417; MUID:84111554; PMID:6319386
A;Accession: A25417
A;Molecule type: protein
A;Residues: 201-259; 'C', 261-281; 'ND', 284-301 <DRI>
C;Comment: Calcium is required for ligand binding.
C;Superfamily: hepatic lectin; C-type lectin homology
C;Keywords: endocytosis; glycoprotein; lectin; liver; receptor; transmembrane protein
F;2-60/Domain: intracellular #status predicted <IN>
F;61-77/Domain: transmembrane #status predicted <TRN>
F;78-301/Domain: extracellular #status predicted <EXT>
F;170-293/Domain: C-type lectin homology <LCH>
F;97,119,165/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.0%; Score 165.5; DB 1; Length 301;
Best Local Similarity 27.3%; Pred. No. 4.4e-08;
Matches 39; Conservative 22; Mismatches 67; Indels 15; Gaps 3;

QY 58 RFLCCGSGKGMFCQSRCPNLWNRNGSHCYFYSMEKRDVNSLSLKFCADKGGSHLLTFPDNQ 117
Db 153 RFLFCQLAFLNSGTETCCPVNWFEGGSCYFWSRDLGTWAEADQYCCWENAHLLVINSRE 212
QY 118 GVNLFEYVGEDFWIGLRIDTG-WRWEDGPALSLSLSNSVQ-----KCG 163
Db 213 EQEFVWKRGAFHWIIGLTDKSGWKVVDGTEYRSFNKNAFTQPDNQWQHEGGSDECA 272
```

QY 164 THRCGL-HASCEVALOWICEK 185
 Db 273 EILSDGLWDFNFCQVNRWACER 295

RESULT 8
 T28140
 natural killer cell receptor homolog - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T28140
 R:Milne, S.; Kaufman, J.; Beck, S.
 A:Description: DNA sequencing and analysis of the chicken major histocompatibility complex
 A:Reference number: Z20475
 A:Accession: T28140
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-170 <MIL>
 A:Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292544; PIDN:CAA18960.1
 A:Experimental source: clone CB12
 C:Genetics:
 A:Gene: B-NK
 A:Map position: 16
 A>Note: Intron positions not resolved (incomplete sequence)

Query Match 15.7%; Score 162.5; DB 2; Length 170;
 Best Local Similarity 28.1%; Pred. No. 4.8e-08;
 Matches 34; Conservative 16; Mismatches 60; Indels 11; Gaps 3;

QY 72 CSRCNLWRNGSHCYFYSMEKRDWNSLKFCADKSGHLLTPPDNQGNLFQFYVGEDFY 131
 Db 47 CLLCPQFWLLGDRCYELSTEGKNTQAKMKCNLSQSLAVLRKKAEDHLLQAGAEVP 106

QY 132 WIGLR-DIDGWEDEGPAL-----SLSLNSVVKCGTHRCGLHASCEVALOWICEK 184
 Db 107 WIGLEVSUNQMKWDNSYNSTESDNLVSMEN---RCGTFKNTKVEGDVCSGERQWVCQ 162

QY 185 K 185
 Db 163 K 163

RESULT 9
 C46467
 NKRP-P1 protein homolog Gene-40 - mouse
 N:Alternate names: natural killer cell activation molecule; NK1.1 alloantigen
 C:Species: Mus musculus (house mouse)
 C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
 C:Accession: C46467; A46499
 R:Giorda, R.; Trucco, M.
 J. Immunol. 147, 1701-1708, 1991
 A:Title: A family of genes selectively coexpressed in adherent lymphokine-activated killer cells
 A:Reference number: A46467; MUID:91349596; PMID:1880421
 A:Accession: C46467
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-220 <GIO>
 A:Cross-references: GB:M77678; NID:g200062; PIDN:AAA39824.1; PID:g200063
 A:Experimental source: NK cells, C57BL/7B
 A>Note: sequence extracted from NCBI backbone (NCBIN:52382, NCBI:P:52383)
 R:Ryan, J.C.; Turck, J.; Niemi, E.C.; Yokoyama, W.M.; Seaman, W.E.
 J. Immunol. 149, 1631-1635, 1992
 A:Title: Molecular cloning of the NK1.1 antigen, a member of the NKRP-P1 family of natural killer cell receptors
 A:Reference number: A46499; MUID:92373004; PMID:1506685
 A:Accession: A46499
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-86, 90-220 <RYA>
 A:Cross-references: GB:S43141; NID:g254094; PIDN:AAB22979.1; PID:g254095
 A:Experimental source: C57BL/6J NK cells
 A>Note: sequence extracted from NCBI backbone (NCBIN:111622, NCBI:P:111624)
 C:Superfamily: natural killer cell receptor P1; C-type lectin homology

C:Keywords: transmembrane protein
 F:91-207/Domain: C-type lectin homology <LCH>

Query Match 15.4%; Score 159.5; DB 2; Length 220;
 Best Local Similarity 25.3%; Pred. No. 1.2e-07;
 Matches 46; Conservative 33; Mismatches 74; Indels 29; Gaps 8;

QY 27 KAVLHRPCVSLVMVALGLLTIVILMSLLY-----QRTLCGSKGFCMCSQCSR----- 74
 Db 38 RLALKLSACGLILLV---LTLIGMSVLVRVLVQKPSREKCC---VFIQENLNKTTVNLE 90

QY 75 CENLWRNGSHCYFYSMEKRDWNSLKFCADKSGHLLTPPDNQGNLFQFYVGEDF--YW 132
 Db 91 CFQDMLLRHDKCFHVSQVSNWEEQADCGRGATLLIQDEELRFLDSIKEXNSFW 150

QY 133 IGLR-----DIDGWEDEGPALSLSLNSVVKQ---CGTHRCGLHASCEVALOWICEK 185
 Db 151 IGLRFTLPDMN-WKWINGTTFNSDVLKITGTENGSCASILGDKVTPSCASDNRWICQK 209

QY 186 VL 187
 Db 210 EL 211

RESULT 10

A35917
 NK-cell receptor P1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1999
 C:Accession: A35917
 R:Giorda, R.; Rudert, W.A.; Vavassori, C.; Chambers, W.H.; Hiserodt, J.C.; Trucco, M.
 Science 249, 1298-1300, 1990
 A:Title: NKRP-P1, a signal transduction molecule on natural killer cells.
 A:Reference number: A35917; MUID:90378305; PMID:2399464
 A:Accession: A35917
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-223 <GIO>
 A:Cross-references: GB:M62891; NID:g205722; PIDN:AAA41710.1; PID:g205723
 C:Superfamily: natural killer cell receptor P1; C-type lectin homology
 C:Keywords: transmembrane protein
 F:94-210/Domain: C-type lectin homology <LCH>

Query Match

15.4%; Score 159.5; DB 2; Length 223;
 Best Local Similarity 23.5%; Pred. No. 1.2e-07;
 Matches 39; Conservative 33; Mismatches 73; Indels 21; Gaps 5;

QY 38 LVMVALGLLTIVILMS-----LLLYQRTLCGSKGFCMCSQCSRCPNLWRNGSHCYYP 89
 Db 54 LALVGMSTLVRVLVQKPSVEPCRVLIQENLSKTGSPAKL-----KCPKDWLSHRDKCFHV 108

QY 90 SMEKRDWNSLKFCADKSGHLLTPPDNQGNLFQFYVGG--EDFYWIGLR---DIDGWE 144
 Db 109 SQTSTWKESLADCGGKATLLVQDQDEELRFLNLTKRISSEFWIGLSYTLSDENWKVI 168

QY 145 DGPALS---LSILNSVVKCGTHRCGLHASCEVALOWICEKVL 187
 Db 169 NGSTLNSDVLSTGTEKDSQVSKVLSQKVLSECDSDNIWVCQEL 214

RESULT 11

S13165
 asialoglycoprotein receptor - mouse
 N:Alternate names: hepatic lectin
 C:Species: Mus musculus (house mouse)
 C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
 C:Accession: S13165
 R:Sanford, J.P.; Doyle, D.
 Biochim. Biophys. Acta 1087, 259-261, 1990
 A:Title: Mouse asialoglycoprotein receptor cDNA sequence: conservation of receptor gene
 A:Reference number: S13165; MUID:91027942; PMID:2223888
 A:Accession: S13165
 A:Molecule type: mRNA

[illegible]

F:153-276/Domain: C-type lectin homology <LCH>

```
Query Match      15.1%; Score 156; DB 2; Length 284;
Best Local Similarity 25.6%; Pred. No. 3.2e-07;
Matches 41; Conservative 20; Mismatches 75; Indels 24; Gaps 4;

QY 52 SLLYQRTLCGSKGFC-----SQSRCPNLWRNGSHCYFMSMEKRDWNSILKF 102
   ||||: : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 SLLHVKQLVSDVRSLSQMAAFRCNGSERTCCPINWVEYEGSCYFSSVFPWTEADKY 180

QY 103 CADKSHLLTFPDNQGVLNFQYVGEDFYWIGLRDIDG-WRWEDGPALSLSILS----- 155
   | : : ||: : : : : : : : : : : : : : : : : : : : : : :
Db 181 COLENAHLVVTSRDEQNFLORHMGPLNTWIGLTQNGFPKWVDGTDYETGFQNRPEQP 240

QY 156 -NSVVQKCGTIHRCGLHASS-----CEVALQWICEKVL 187
   | : : : : : : : : : : : : : : : : : : : : : : :
Db 241 DNWYGHGLGGEDCAHFTTDGGRWDDVCRRPYRWVCETKL 280
```

Search completed: August 10, 2004, 16:19:36
Job time : 11.9788 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:05:41 ; Search time 7.32035 Seconds

(without alignments)
1337.256 Million cell updates/sec

Title: US-09-811-367B-5

Perfect score: 1036

Sequence: 1 MADNSIYSTLELPAAPRVQD.....GLHASCEVALQWICEKVLP 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	184.5	17.8	199	1	CD69 HUMAN
2	172.5	16.7	227	1	P27811 mus musculus
3	167	16.1	223	1	NK112 MOUSE
4	163.5	15.8	179	1	Q8mzx9 macaca mula
5	161.5	15.6	301	1	LECI1 RAT
6	159.5	15.4	223	1	NK14 MOUSE
7	159.5	15.4	223	1	NK13 RAT
8	159.5	15.4	201	1	LECI1 MOUSE
9	159	15.3	216	1	NRKGD MACMU
10	157	15.2	216	1	NRKGD HUMAN
11	155	15.0	179	1	CD94 HUMAN
12	155	15.0	179	1	CD94 PANTR
13	154.5	14.9	304	1	MMGL MOUSE
14	154	14.9	163	1	V239 FOWPV
15	154	14.9	199	1	CD69 MOUSE
16	154	14.9	283	1	LECH MOUSE
17	153.5	14.8	149	1	CLE2 HUMAN
18	152	14.7	240	1	NRKGE PANTR
19	149.5	14.4	233	1	NKGA PANTR
20	148.5	14.3	133	1	RMCA AGKRH
21	148.5	14.3	306	1	MMGL RAT
22	143.5	13.9	233	1	NKGA MACMU
23	142.5	13.8	233	1	NKGA HUMAN
24	142.5	13.8	359	1	CD72 HUMAN
25	140.5	13.6	148	1	CVXB CRODU
26	140.5	13.6	233	1	NKGC PANTR
27	140.5	13.6	311	1	LECI1 HUMAN
28	139.5	13.5	1722	1	LY75 HUMAN
29	139	13.4	240	1	NRKGE HUMAN
30	139	13.4	283	1	LECH RAT
31	137	13.2	167	1	V008 FOWPV
32	136.5	13.2	207	1	LECH CHICK
33	134.5	13.0	231	1	NKGC MACMU

34	134	12.9	290	1	LECH HUMAN
35	134	12.9	548	1	KUCR MOUSE
36	134	12.9	2738	1	PGCV RAT
37	134	12.9	3358	1	PGCV MOUSE
38	133.5	12.9	231	1	NKGC HUMAN
39	132.5	12.8	117	1	CHBB CROHO
40	132.5	12.8	1458	1	PA2R RABIT
41	131	12.6	157	1	MMHA AGKHA
42	131	12.6	331	1	FCE2 MOUSE
43	131	12.6	550	1	KUCR RAT
44	131	12.6	3381	1	PGCV BOVIN
45	130	12.5	146	1	MMHB AGKHA

P07306	homo sapien
P70194	mus musculus
Q9erb4	rattus norv
Q62059	mus musculus
P26717	homo sapien
P81509	crotalus ho
P49260	oryctolagus
Q9ygg9	agkistrodon
P20693	mus musculus
P10716	rattus norv
P81282	bos taurus
Q9yi92	agkistrodon

ALIGNMENTS

RESULT 1					
CD69_HUMAN					
ID CD69_HUMAN	STANDARD;	PRT;	199 AA.		
AC Q07108;					
DT 01-OCT-1994	(Rel. 30, Created)				
DT 01-OCT-1994	(Rel. 30, Last sequence update)				
DT 15-MAR-2004	(Rel. 43, Last annotation update)				
DE Early activation antigen CD69	(Early T-cell activation antigen p60)				
DE (GP32/28) (Ileu-23) (MLR-3) (EAL)	(BL-AC/P26) (Activation inducer molecule) (AIM).				
DE CB69.					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX NCBI_TaxID=9606;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC TISSUE=Blood;					
RX MEDLINE=93267093; PubMed=8496594;					
RA Hamann J., Fiebig H., Strauss M.;					
RA "Expression cloning of the early activation antigen CD69, a type II					
RT integral membrane protein with a C-type lectin domain.";					
RL J. Immunol. 150:4920-4927 (1993).					
RN [2]					
RP SEQUENCE FROM N.A., AND SEQUENCE OF 96-103; 128-146 AND 189-199.					
RC TISSUE=Blood;					
RX MEDLINE=93340630; PubMed=8340758;					
RA Lopez-Cabrera M., Santis A.G., Fernandez-Ruiz E., Blacher R.,					
RA Esch F., Sanchez-Mateos P., Sanchez-Madrid F.;					
RT "Molecular cloning, expression, and chromosomal localization of the					
RT human earliest lymphocyte activation antigen AIM/CD69, a new member					
RT of the C-type animal lectin superfamily of signal-transmitting					
RT receptors.";					
RL J. Exp. Med. 178:537-547 (1993).					
RN [3]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=93314711; PubMed=8100776;					
RA Ziegler S.F., Ramsdell F., Hjerrild K.A., Armitage R.J.,					
RA Grabstein K.H., Hennen K.B., Farrah T., Fanslow W.C., Shevach E.M.,					
RA Alderson M.R.;					
RT "Molecular characterization of the early activation antigen CD69: a					
RT type II membrane glycoprotein related to a family of natural killer					
RT cell activation antigens.";					
RL Eur. J. Immunol. 23:1643-1648 (1993).					
RN [4]					
RP SEQUENCE FROM N.A.					
RC TISSUE=Placenta;					
RX MEDLINE=94298875; PubMed=8026529;					
RA Santis A., Lopez-Cabrera M., Hamann J., Strauss M., Sanchez-Madrid F.;					
RT "Structure of the gene coding for the human early lymphocyte					
RT activation antigen CD69: a C-type lectin receptor evolutionarily					
RT related with the gene families of natural killer cell-specific					
RT receptors.";					
RL Eur. J. Immunol. 24:1692-1697 (1994).					
RN [5]					
RP SEQUENCE FROM N.A.					

RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallamy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Involved in lymphocyte proliferation and functions as a
CC signal transducing receptor in lymphocytes, natural killer (NK)
CC cells, and platelets.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed on the surface of activated T-cells,
CC B-cells, natural killer cells, neutrophils, eosinophils, epidermal
CC Langerhans cells and platelets.
CC -!- DEVELOPMENTAL STAGE: Earliest inducible cell surface glycoprotein
CC acquired during lymphoid activation.
CC -!- INDUCTION: By antigens, mitogens or activators of PKC on the
CC surface of T and B lymphocytes. By interaction of IL-2 with the
CC p75 IL-2R on the surface of NK cells.
CC -!- PTM: CONSTITUTIVE SER/THR PHOSPHORYLATION IN BOTH MATURE
CC THYMOCYTES AND ACTIVATED T LYMPHOCYTES.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- DATABASE: NAME=PRO; NOTE=CD guide CD69 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd69.htm".
CC
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CC
CC EMBL; L07555; AAB46359.1; -
CC EMBL; Z22576; CAA80298.1; -
CC EMBL; Z30426; CAA83017.1; -
CC EMBL; Z30430; CAA83017.1; JOINED.
CC EMBL; Z30427; CAA83017.1; JOINED.
CC EMBL; Z30429; CAA83017.1; JOINED.
CC EMBL; Z30428; CAA83017.1; JOINED.
CC EMBL; BC007037; AAH07037.1; -
CC PIR; JH0822; JH0822.
CC PDB; 1E87; 18-JUL-03.
CC PDB; 1E81; 18-JUL-03.
CC Genew; HGNC:1694; CD69.
CC MIM; 107273; -
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC DR; GO:0004888; F:transmembrane receptor activity; TAS.
CC InterPro; IPR001304; Lectin_C.
CC Pfam; PF00059; lectin_c; 1.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C TYPE LECTIN 1; FALSE_NEG.
CC PROSITE; PS50041; C TYPE LECTIN 2; 1.
CC Antigen; Signal-anchor; Transmembrane; Lectin; Glycoprotein;
CC Phosphorylation; 3D-structure.
CC DOMAIN 1 40 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 41 61 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT

FT DOMAIN 62 199 (POTENTIAL).
FT DOMAIN 92 195 EXTRACELLULAR (POTENTIAL).
FT DISULFID 68 85 C-TYPE LECTIN.
FT DISULFID 96 194 BY SIMILARITY.
FT DISULFID 173 186 BY SIMILARITY.
FT CARBOHYD 166 166 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 199 AA; 22559 MW; 172E2699D2FB8DFB CRC64;
Query Match 17.8%; Score 184.5; DB 1; Length 199;
Best Local Similarity 26.3%; Pred. No. 4.5e-11;
Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;
QY 35 VSYLVVVALGHLTVLMSLLLYQRTLCGSGKGMV---SQGSRCPNLMWRNGSHCYFESM 91
DB 45 VNVVVFITLIIALISVGGIN---CPGQVTFSPSHVSSCEDWVGQKCYFIST 101
QY 92 EKRDWNSLKFCADKAGSHLLTFPNQGVNLPQEVYGVDFYWIGRLDIDG--WRWEDGPA 149
DB 102 VKRSWTSQAQACSEHGATLAVIDSEKDMNFKRYAGREHVVGLKKEPHEWKSNGKEF 161
QY 150 SLSILSNSVQKGTIHRGGLHASSCEVALOWICEK 185
DB 162 N-NMFNVTGDKCVFLKNTVESSMECEKNLYWICNK 196

RESULT 2
NK11 MOUSE
ID NK11_MOUSE STANDARD; PRT; 227 AA.
AC P27811;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Natural killer cell surface protein P1-2 (NKR-P1 2) (NKR-P1.7).
GN KLRB1A OR LY55A OR LY55.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91349596; PubMed=1880421;
RA Giorda R., Trucco M.;
RT "Mouse NKR-P1. A family of genes selectively coexpressed in adherent
RT lymphokine-activated killer cells.";
RL J. Immunol. 147:1701-1708(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92013158; PubMed=1680927;
RA Yokoyama W.M., Ryan J.C., Hunter J.J., Smith H.R.C., Stark M.,
RA Seaman W.E.;
RT "cDNA cloning of mouse NKR-P1 and genetic linkage with LY-49.
RT Identification of a natural killer cell gene complex on mouse
RT chromosome 6.";
RL J. Immunol. 147:3229-3236(1991).
CC -!- FUNCTION: May function as signal-transmitting receptor.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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CC
CC EMBL; M7676; AAA39822.1; -
CC EMBL; M7753; AAA39366.1; -
CC PIR; A46457; A46457.
CC HSPF; P22897; 1EGG.

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DR MGD; MGI:107540; KIRb1a.
DR InterPro; IPR002353; AntifreezeZell.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 43 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 63 227 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 93 212 C-TYPE LECTIN (LONG FORM).
FT DISULFID 94 105 BY SIMILARITY.
FT DISULFID 122 210 BY SIMILARITY.
FT DISULFID 189 202 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 39 39 S -> L (IN REF. 2).
SQ SEQUENCE 227 AA; 25689 MW; 0599A2587DF0B615 CRC64;

Query Match 16.7%; Score 172.5; DB 1; Length 227;
Best Local Similarity 24.4%; Pred. No. 7.9e-10;
Matches 53; Conservative 35; Mismatches 86; Indels 43; Gaps 8;

QY 6 IYSTLELPAAPRVQDDSRWKV-----KAVLHRPCVSYLVWVALGGLLVLMGLL 54
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 VYGLKPPRTPGAWHESPSPSLPPDACRCPSHRSLKSLCAGLLLV-----VTLLGMSVL 61
Y 55 -----LYQRTLCCKSGKGFMCSCRCPNLWNRNGSHCYFYSMEKRDWNSL 99
D 62 VRVLIQPSIEKCVLVQENL---NKTTCDSAKLECPQDWLSHRDKCFHVSQVSNWTBERG 118
Y 100 LKFCADKGSLLTFFPDNQGVLNFOEYVGEDF--YWTGLR-----DIDGWEDGPALS--- 150
D 119 LVDCDGKATLMLQDQEELRFLDSIKEKNSFWIGRLYTLFDMN-WKWLNGSTLNSDV 177
Y 151 LSILNSVVKCGTTHRCGLHASSCEVALQWICEKVL 187
D 178 LKITGDTENDSCAALSGDKVTFESCNSDNRWICQKEL 214

RESULT 3
NK12 MOUSE
ID NK12 MOUSE STANDARD; PRT; 223 AA.
AC P27812;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE Natural killer cell surface protein P1-34 (NKR-P1 34).
GN KLRB1B OR LY55B OR LY55-B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91349596; PubMed=1880421;
RA Giordano R., Trucco M.;
RT "Mouse NKR-P1. A family of genes selectively coexpressed in adherent
RL lymphokine-activated killer cells.";
RL J. Immunol. 147:1701-1708(1991).
RN [2]
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=92388663; PubMed=1517565;
RA Giordano R., Weisberg E.P., Ip T.K., Trucco M.;
RT "Genomic structure and strain-specific expression of the natural
RT killer cell receptor NKR-P1."
RL J. Immunol. 149:1957-1963(1992).
CC -!- FUNCTION: May function as signal-transmitting receptor.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.

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CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
DR EMBL; M77677; AAA39823.1; -.
DR EMBL; X64721; CAA45974.1; -.
DR PIR; B46467; B46467.
DR MGD; MGI:107539; KIRb1b.
DR InterPro; IPR002353; AntifreezeZell.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
FT DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 44 63 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 64 223 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 93 212 C-TYPE LECTIN (LONG FORM).
FT DISULFID 94 105 BY SIMILARITY.
FT DISULFID 122 210 BY SIMILARITY.
FT DISULFID 189 202 BY SIMILARITY.
FT CARBOHYD 81 81 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 223 AA; 25157 MW; 8D04C11DEB89C56 CRC64;

Query Match 16.1%; Score 167; DB 1; Length 223;
Best Local Similarity 23.3%; Pred. No. 2.7e-09;
Matches 50; Conservative 34; Mismatches 91; Indels 40; Gaps 8;

QY 6 IYSTLELPAAPRVQDDSD-----RWKVAVLHRPCVSY-----LVWVALGGLL 46
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 VYADNLARIQEPKHDSPPSLPDTCCRPW-----HRLAKFGCAGLLLVLVVIGLC 60
Y 47 TVIIMSLLYQRTLCG-----SKGFMCSCRCPNLWNRNGSHCYFYSMEKRDWNSL 101
D 61 VLVLVQKSSVQKICADVQENRTHTTDCSVNLECPQDWLSHRDKCFRVQVSNWTBERGQA 120
Y 102 FCADKGSLLTFFPDNQGVLNFOEYVGEDF--YWTGLR-----DIDGWEDGPALS---LS 152
D 121 DCGRKGATLLLIQDQEELRFLDSIKEKNSFWIGRLYTLFDMN-WKWLNGSTLNSDV 179
Y 153 ILNSVVKCGTTHRCGLHASSCEVALQWICEKVL 187
D 180 ITGDTENGSCASISGDKVTFESCNSDNRWICQKEL 214

RESULT 4
CD94 MACMU
ID CD94 MACMU STANDARD; PRT; 179 AA.
AC Q9WK9; Q9WK9; Q9WK9; Q9WK9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Natural killer cells antigen CD94 (NK cell receptor) (killer cell
DE lectin-like receptor subfamily D, member 1).
GN KLRD1 OR CD94.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OC NCBI_taxid=9544;
RN [1]

```

SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 MEDLINE=20322487; PubMed=10866118;
 LeBonte M.L., Levy D.B., Letvin N.L.;
 "Characterization of rhesus monkey CD94/NGK2 family members and
 identification of novel transmembrane-deleted forms of NK2-A, B, C,
 and D.";
 Immunogenetics 51:496-499 (2000).
 [2]
 SEQUENCE FROM N.A. (ISOFORM 1).
 MEDLINE=21158386; PubMed=11261935;
 Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.;
 "Selective expression of NK2-A and NK2-C mRNAs and novel alternative
 splicing of 5' exons in rhesus monkey decidua.";
 Immunogenetics 53:69-73 (2001).
 CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
 class I HLA-E molecules by NK cells and some cytotoxic T-cells.
 CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NK2 family
 members.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=CD94-A;
 CC IsoId=Q9MK9-1; Sequence=Displayed;
 CC Name=2; Synonyms=CD94-B;
 CC IsoId=Q9MK9-2; Sequence=VSP_003055;
 CC Name=3; Synonyms=CD94 alt;
 CC IsoId=Q9MK9-3; Sequence=VSP_003054;
 CC -!- TISSUE SPECIFICITY: Natural killer cells.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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 DR EMBL; AF190931; AAF74527.1; -
 DR EMBL; AF190932; AAF74528.1; -
 DR EMBL; AF190933; AAF74529.1; -
 DR EMBL; AF294886; AAG34498.1; -
 DR HSSP; P22897; 1EGG.
 DR InterPro; IPR001304; Lectin C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT_1.
 DR PROSITE; PS00615; C TYPE LECTIN 1; FALSE NEG.
 DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
 KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
 KW Alternative splicing; Polymorphism.
 FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT FT
 FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 61 72 BY SIMILARITY.
 FT DISULFID 89 174 BY SIMILARITY.
 FT DISULFID 152 166 BY SIMILARITY.
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPPLIC 1 34 MAVFKTLWRLISGTGICSLMATGILKNS -> MAA
 (in isoform 3).
 FT FT
 FT VARSPPLIC 105 105 /FTID=VSP_003054.
 FT FT
 FT VARIANT 139 139 L -> LQ (in isoform 2).
 FT FT
 FT SEQUENCE 179 AA; 20607 MW; 06212B4494527F07 CRC64;
 Y -> D.
 Query Match 15.8%; Score 163.5; DB 1; Length 179;
 Best Local Similarity 31.2%; Pred. No. 4.7e-09;
 Matches 39; Conservative 19; Mismatches 58; Indels 9; Gaps 4;
 70 SOCSRCPNLWRNGSHCYFSMEKRDWNSLSKFCADKGSLLTFFPDNGQVNLFBQBYVGED 129

Db 56 SDCCSCHEKVGVCNCYFISSEKRWESRHFCSQKSSLLQLQNRDELDFMSS--SQH 113
 QY 130 FWIGL---RDIDGWRWDGPPALSILSNSVVK---CGTHRCG-LHASCEVALQWI 182
 Db 114 FYWIGLSSEHTAWLWENGSAISOYLPFFSEFTFRKQNCIAYNSKGNALDESCETKNRYI 173
 QY 183 CEKVL 187
 Db 174 CKQL 178
 RESULT 5
 LECTIN RAT
 ID LECTIN RAT STANDARD; PRT; 301 AA.
 AC P08290;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Asialoglycoprotein receptor R2/3 (Hepatic lectin 2/3) (RHL-2) (ASGP-R)
 DE (ASGP-R)
 GN ASGR2 OR ASGR-2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87257885; PubMed=3600647;
 RA McPhaul M., Berg P.;
 RT "Identification and characterization of cDNA clones encoding two
 RT homologous proteins that are part of the asialoglycoprotein
 RT receptor.";
 RL Mol. Cell. Biol. 7:1841-1847(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87250656; PubMed=3597443;
 RA Halberg D.F., Wager R.E., Farrell D.C., Hildreth J., Quesenberry M.S.,
 RA Loeb J.A., Holland E.C., Drickamer K.;
 RT "Major and minor forms of the rat liver asialoglycoprotein receptor
 RT are independent galactose-binding proteins. Primary structure and
 RT glycosylation heterogeneity of minor receptor forms.";
 RL J. Biol. Chem. 262:9828-9838(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=89170119; PubMed=3234178;
 RA Sanford J.P., Elliott R.W., Doyle D.;
 RT "Asialoglycoprotein receptor genes are linked on chromosome 11 in the
 RT mouse.";
 RL DNA 7:721-728(1988).
 RN [4]
 RP SEQUENCE OF 201-301.
 RX MEDLINE=84111554; PubMed=6319386;
 RA Drickamer K., Mamon J.F., Binns G., Leung J.O.;
 RT "Primary structure of the rat liver asialoglycoprotein receptor.
 RT Structural evidence for multiple polypeptide species.";
 RL J. Biol. Chem. 259:770-778(1984).
 CC -!- FUNCTION: Mediates the endocytosis of plasma glycoproteins to
 CC which the terminal sialic acid residue on their complex
 CC carbohydrate moieties has been removed. The receptor recognizes
 CC terminal galactose and N-acetylgalactosamine units. After ligand
 CC binding to the receptor, the resulting complex is internalized and
 CC transported to a sorting organelle, where receptor and ligand are
 CC disassociated. The receptor then returns to the cell membrane
 CC surface.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed exclusively in hepatic parenchymal
 CC cells.
 CC -!- MISCELLANEOUS: Calcium is required for ligand binding.
 CC -!- MISCELLANEOUS: Two types of rat hepatic lectin have been
 CC identified, RHL-1 and RHL-2/3, having a relative abundance of 4:1.
 CC RHL-2 and RHL-3 only differs in their carbohydrate structures.

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CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M16347; AAA42038.1; -.
CC EMBL; J02762; AAA41522.1; -.
CC EMBL; X07636; CAA30476.1; -.
CC PIR; B28462; LNR12.
CC HSP; P06734; IHL1.
CC InterPro; IPR002353; AntifreezeII.
CC InterPro; IPR001304; lectin_C.
CC InterPro; IPR005640; lectin_N.
CC Pfam; PF00059; lectin_C; 1.
CC Pfam; PF03954; lectin_N; 1.
CC PRINTS; PR00356; ANTIFREEZEII.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
CC PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
CC Lactin; Glycoprotein; Receptor; Endocytosis; Transmembrane;
KW Calcium; Signal-anchor; Phosphorylation.
FT DOMAIN 1 58 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 59 79 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 80 301 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 169 295 C-TYPE LECTIN (LONG FORM).
FT DISULFID 170 181 BY SIMILARITY.
FT DISULFID 198 293 BY SIMILARITY.
FT DISULFID 271 285 BY SIMILARITY.
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .).
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .).
FT CONFLICT 153 153 R -> A (IN REF. 1).
FT CONFLICT 202 202 I -> N (IN REF. 2 AND 3).
FT CONFLICT 260 260 C -> W (IN REF. 2 AND 3).
SQ SEQUENCE 301 AA; 34943 MW; 3C2315E642D71279 CRC64;

Query Match 15.6%; Score 161.5; DB 1; Length 301;
Best Local Similarity 27.3%; Pred. No. 1.3e-08;
Matches 39; Conservative 22; Mismatches 67; Indels 15; Gaps 3;

Qy 58 RTLCGSKGFMCSQCSRCPNLWMRNGSHCYFYSMEKRDWNSLKFCDKSGHLLTFFPDNQ 117
Db 153 RLTLCQLAFSLNSGTECCPVNWFVGGSCYFSDGLTWAEDQYCWMEIAHLVINSRE 212
Qy 118 GVNLFQYVGEDFWIGLRIDIG-WRWEDGSPALSILSVVQ-----KCG 163
Db 213 EQEFVWKRGAFTWIGLTDKSGWKVGDGYEYSNFKNWAFTQPDNCQHEGGSEDCA 272
Qy 164 TIHRCGH-HASSCEVALQWICEK 185
Db 273 EILSDGLWNDNFCCQVNRWACER 295

RESULT 6
NK14_MOUSE
ID NK14_MOUSE STANDARD; PRT; 220 AA.
AC P27814;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Natural killer cell surface protein P1-40 (NKR-P1 40) (NKR-P1.9).
GN KLR1C OR LY55C OR LY55-C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=91349596; PubMed=1880421;
RA Giorda R., Trucco M.;
RT "Mouse NKR-P1. A family of genes selectively coexpressed in adherent
RT lymphokine-activated killer cells.";
RL J. Immunol. 147:1701-1708(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=92373004; PubMed=1506685;
RA Ryan J.C., Turck J., Niemi E.C., Yokoyama W.M., Seaman W.E.;
RT "Molecular cloning of the NK1.1 antigen, a member of the NKR-P1
RT family of natural killer cell activation molecules.";
RL J. Immunol. 149:1631-1635(1992).
RN [2]
CC -1- FUNCTION: May function as signal-transmitting receptor.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- TISSUE SPECIFICITY: Natural killer cells.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
CC EMBL; M77678; AAA39824.1; -.
CC PIR; C46467; C46467.
CC SWISS-2DPAGE; P27814; MOUSE.
CC MGD; MGI:107538; Klr1c.
CC InterPro; IPR002353; AntifreezeII.
CC InterPro; IPR001304; lectin_C.
CC Pfam; PF00059; lectin_C; 1.
CC PRINTS; PR00356; ANTIFREEZEII.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
CC PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 43 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 63 220 EXTRACELLULAR (POTENTIAL).
FT DISULFID 90 212 C-TYPE LECTIN (LONG FORM).
FT DISULFID 119 207 BY SIMILARITY.
FT DISULFID 186 199 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 220 AA; 24771 MW; 8A160B1DED46398F CRC64;

Query Match 15.4%; Score 159.5; DB 1; Length 220;
Best Local Similarity 25.3%; Pred. No. 1.5e-08;
Matches 46; Conservative 33; Mismatches 74; Indels 29; Gaps 8;

Qy 27 KAVLHRCVSVLVVVALGLTLVILMSLLY-----QRTLCGSKGFMCSQCSR----- 74
Db 38 RLALKLSGAGLLIV-----LTLIGMSVLVRLVQKPSREKCC---VFQENLAKTIVNLE 90
Qy 75 CPNLWMRNGSHCYFYSMEKRDWNSLKFCDKSGHLLTFFPDNQVNLQFQVVGEDF--YW 132
Db 91 CPQDWLHLRDKCFHVSQVSNVWEEGQADCGKRGATLLIQDBELRFLDSIKEKYNFW 150
Qy 133 IGLR----DIDGWRWEDGPALSILSVVQK---CGTIHRCGLHASSCEVALQWICEK 185
Db 151 IGLRFTLPDMN-WKWINGTTFNSDLVLTGVTENGSCASILGDKVTFESCADNRWLQCK 209
Qy 186 VL 187
Db 210 EL 211
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RESULT 7
ID NK13 RAT STANDARD; PRT; 223 AA.
AC P27471
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Natural killer cell surface protein PI-3.2.3 (NKR-PI 3.2.3) (Antigen
DE 3.2.3).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90378305; PubMed=2399454;
RA Giordano R., Rudert W.A., Vavassori C., Chambers W.H.,
RA Hiserodt J.C., Trucco M.;
RT "NKR-PI, a signal transduction molecule on natural killer cells.";
RL Science 249:1298-1300(1990).
CC -!- FUNCTION: Mediates transmembrane signaling in natural killer
CC (NK) cells and so may act as a receptor able to selectively
CC trigger NK cell activity.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- MISCELLANEOUS: Ligand binding may be calcium dependent.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
DR EMBL; M62891; AAA41710.1; .
DR PIR; A35917; A35917.
DR HSP; P22897; 1EG3.
DR InterPro; IPR002353; AntifreezeII.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE LECTIN 2; 1.
KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
FT DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 44 63 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 64 223 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 93 212 C-TYPE LECTIN (LONG FORM).
FT DISULFID 94 105 BY SIMILARITY.
FT DISULFID 122 210 BY SIMILARITY.
FT DISULFID 189 202 BY SIMILARITY.
FT CARBOHYD 82 82 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 223 AA; 24551 MW; FCD12B212DDF4330 CRC64;

Query Match 15.4%; Score 159.5; DB 1; Length 223;
Best Local Similarity 23.5%; Pred. No. 1.5e-08;
Matches 39; Conservative 33; Mismatches 73; Indels 21; Gaps 5;

QY 38 LVMVALGLLTVLMS-----LLLYQRTLCCKSGKQSCPCNPLWRNGHCYFF 89
DB 54 LALVQMSILVRVLVQKPSVEPCRLVQLQENLTKTSPAKL-----KCPKDWLSHRDKCFHV 108
QY 90 SMEKRDWNSLKFCAADKSHLLTFPDNQGVLNFBQYVG--EDFYVIGLR---DIDGWRWE 144
DB 109 SQTSTITWKESLADCGKGATLLLVQDELPRLNLTFRISSSFVIGLSYLTSDENWKVI 168

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QY 145 DGPALSDVVKCGTTHRCGLHASSCEVALQWICKEVL 187
DB 169 NGSTLNSDVLSTGTGDKSDCASVQDKVLSECDSDNIWVQCKEL 214

RESULT 8
ID LECI MOUSE STANDARD; PRT; 301 AA.
AC P24721
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Asialoglycoprotein receptor 2 (Hepatic lectin 2) (MHL-2) (ASGP-R)
DE (ASGPR).
GN ASGP2 OR ASGP-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=91027942; PubMed=2223888;
RA Sanford J.P., Doyle D.;
RT "Mouse asialoglycoprotein receptor cDNA sequence: conservation of
RL receptor genes during mammalian evolution.";
RL Biochim. Biophys. Acta 1087:259-261(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Mediates the endocytosis of plasma glycoproteins to
CC which the terminal sialic acid residue on their complex
CC carbohydrate moieties has been removed. The receptor recognizes
CC terminal galactose and N-acetylgalactosamine units. After ligand
CC binding to the receptor, the resulting complex is internalized and
CC transported to a sorting organelle, where receptor and ligand are
CC disassociated. The receptor then returns to the cell membrane
CC surface.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed exclusively in hepatic parenchymal
CC cells.
CC -!- MISCELLANEOUS: Calcium is required for ligand binding.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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DR EMBL; X53042; CAA37211.1; -.
DR EMBL; BC011197; AH011197.1; -.
DR PIR; S13165; S13165.
DR HSSP; P06734; 1HLI.
DR MGD; MGI:88082; Asgr2.
DR InterPro; IPR002353; Antifreeze2.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR005640; lectin_N.
DR Pfam; PF00059; lectin_C; 1.
DR Pfam; PF03954; lectin_N; 1.
DR PRINTS; PR00356; ANTI-FREEZE1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
KW Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane;
FT DOMAIN 1 58 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 59 79 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 80 301 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 169 295 C-TYPE LECTIN (LONG FORM).
FT DISULFID 170 181 BY SIMILARITY.
FT DISULFID 198 293 BY SIMILARITY.
FT DISULFID 271 285 BY SIMILARITY.
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 301 AA; 34907 MW; 3A29F1AF6A68F298 CRC64;

Query Match 15.4%; Score 159.5; DB 1; Length 301;
Best Local Similarity 26.6%; Pred. No. 2e-08;
Matches 38; Conservative 23; Mismatches 67; Indels 15; Gaps 3;

QY 58 RTLCGSKGFMCSQSRCPNLMWRNGSHCYFYSMEKRDWNSLKFPCADKGSLLTTPDNQ 117
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 153 RTLCQLAYFQSGTECCPVNWFVFGGCVFSGDGLTWAEDQYQLENAHLIVNSRE 212
QY 118 GVNLFQYVGEDEFWIGLRIDG-WRWEDGPAISLSLSNSVVO-----KCG 163
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 213 EQDFVVRKSHQFHWIGLTDGSKWVDGTDYRSNRYNWAFTQPDNMQGHEQGGEDCA 272
QY 164 TIHRCG-LHASSCEVALQWICEK 185
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 273 EILSDGHWNDFCCQVNRWVCEK 295

RESULT 9
NKGD MACMU STANDARD; PRT; 216 AA.
AC Q9WZJ7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE NKG2-D type II integral membrane protein (NKG2-D activating NK
DE receptor) (NK cell receptor D).
GN NKG2D.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20322487; PubMed=10866118;
RA LaBonte M.L., Levy D.B., Letvin N.L.;
RT "Characterization of rhesus monkey CD94/NKG2 family members and
RT identification of novel transmembrane-deleted forms of NKG2-A, B, C,
RT and D.";
RL Immunogenetics 51:496-499(2000).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.

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CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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CC
DR EMBL; AF190943; AAF74539.1; -.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein; Polymorphism.
FT DOMAIN 1 51 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 52 72 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 73 216 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 213 C-TYPE LECTIN (LONG FORM).
FT DISULFID 99 110 BY SIMILARITY.
FT DISULFID 127 211 BY SIMILARITY.
FT DISULFID 189 203 BY SIMILARITY.
FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 216 AA; 25075 MW; A44883F31400DEAC CRC64;

Query Match 15.3%; Score 159; DB 1; Length 216;
Best Local Similarity 26.4%; Pred. No. 1.6e-08;
Matches 43; Conservative 33; Mismatches 59; Indels 28; Gaps 6;

QY 39 VMVALGLLTVILMSL-----LLYQRTLCGSKGFMCSQSRCPNLMWRNGSHCYFYS 90
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 IAVAMGRFIMVTWTSVAFLNSLEFQVQIPUTE-----SYCGPCPKNWKCYKNKCYQFF 114
QY 91 MEKRDWNSLKFPCADKGSLLTTPDNQGVNLFQYVGEDEFWIGLRDI---DGRWRWDGDP 147
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 NESKNWVESQASCSQNASLLKYVSKEDQDLLK--LVKSYHVMGLVHIPGTSQWEDGS 172
QY 148 ALSLSLSNSVVOKGTIHRGCLHASS-----CEVALQWIC 183
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 173 ILSPNLLTIEMOK---GDCALYASSFKGYIENCSPNPTIYC 211

RESULT 10
NKGD HUMAN STANDARD; PRT; 216 AA.
ID NKGD_HUMAN
AC P26718; Q9NR41;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE NKG2-D type II integral membrane protein (NKG2-D activating NK
DE receptor) (NK cell receptor D).
GN NKG2D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91178434; PubMed=2007850;
RA Houchins J.P., Yabe T., McSherry C., Bach F.H.;
RT "DNA sequence analysis of NKG2, a family of related cDNA clones
RT encoding type II integral membrane proteins on human natural killer
RT cells.";
RL J. Exp. Med. 173:1017-1020(1991).
RN [2]
RP SEQUENCE FROM N.A.

```


RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RA Blassoni R.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RX MEDLINE=98267245; PubMed=9601951;
 RA Furukawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T., Tadokoro K.,
 RA Tohma S., Inoue T., Yamamoto K., Juji T.;
 RT "A alternatively spliced form of the human CD94 gene.";
 RL Immunogenetics 48:87-88(1998).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Blood;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.F., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Haile S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:116899-116903(2002).
 CC -I- FUNCTION: Plays a role as a receptor for the recognition of MHC
 CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
 CC -I- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
 CC members.
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=CD94-A;
 CC IsoId=Q13241-1; Sequence=Displayed;
 CC Name=2; Synonyms=CD94-B;
 CC IsoId=Q13241-2; Sequence=VSP_003053;
 CC Name=3; Synonyms=CD94 alt;
 CC IsoId=Q13241-3; Sequence=VSP_003052;
 CC -I- TISSUE SPECIFICITY: Natural killer cells.
 CC -I- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -I- DATABASE: NAME=PROW; NOTE=CD guide CD94 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd94.htm".
 CC -----
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 CC -----
 DR EMBL; U30610; AAC50291.1; -;
 DR EMBL; Y14287; CAA74663.1; -;
 DR EMBL; Y14288; CAA74663.1; JOINED.
 DR EMBL; AJ000673; CAA04230.1; -;
 DR EMBL; AJ000001; CAA03845.1; -;
 DR EMBL; AB009597; BAA24450.1; -;
 DR EMBL; AB010084; BAA24451.1; -;
 DR EMBL; BC028009; AAB28009.1; -;
 DR PDB; 1B6E; 15-JUN-99.
 DR Genew; HGNC:6378; KLRD1.
 DR MIM; 602894; -;
 GO; GO:0005886; C:plasma membrane; TAS.

DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
 DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG.
 DR PROSITE; PS00041; C-TYPE LECTIN_2; 1.
 KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
 KW Alternative splicing; 3D-structure.
 FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 98 176 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 61 72 BY SIMILARITY.
 FT DISULFID 89 174 BY SIMILARITY.
 FT DISULFID 152 166 BY SIMILARITY.
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 1 34 MAYFKTLWRLISGTIGTICLSLMAITGILLKNS -> MAA
 FT (in isoform 3).
 FT VARSPLIC 105 105 /FTId=VSP_003052.
 FT L -> IQ (in isoform 2).
 FT /FTId=VSP_003053.
 FT SQ SEQUENCE 179 AA; 20497 MW; 1884D99E8D9583A7 CRC64;
 Query Match 15.0%; Score 155; DB 1; Length 179;
 Best Local Similarity 27.0%; Pred. No. 3.2e-08;
 Matches 47; Conservative 28; Mismatches 85; Indels 14; Gaps 7;
 QY 24 WK-VKAVLHRPCVSYLVMAVGLLTVLMSLLLYQRTLCGSKGFM--CSQSRCPNLMW 80
 DB 9 WRUGISGTGLGICLS--IMATGLILLKNSFTKLSIEPAFTGPNIELQKDDCCSCQEKWV 66
 QY 81 RNSGHCVYFSEMEKRDWNSLKFCAKDGSHLLTFPDNGVNLFORVGEFYWGL--RRD 137
 DB 67 GYRCNCYFISSEQKTWNSRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWGLSYSEE 124
 QY 138 IDGWRMEDGPALSLISLSNV---VQKCGTIHRGG-LHASSCEVALOWICEKVL 187
 DB 125 HTAWLWNGSALSQYLPSPSPFTNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178
 RESULT 12
 ID CD94 PANTR STANDARD; PRT; 179 AA.
 AC QWMZ41;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
 DE lectin-like receptor subfamily D, member 1).
 GN KLRD1 OR CD94.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20350666; PubMed=10894168;
 RA Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,
 RA Muir D.G., Canavez F., Cooper S.L., Valiante N.M., Lanier L.L.,
 RA Parham P.;
 RT "Rapid evolution of NK cell receptor systems demonstrated by
 RT comparison of chimpanzees and humans.";
 RL Immunity 12:687-698(2000).
 RN [2]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=21623889; PubMed=11751968;
 RA Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,
 RA Cleland S., Guethlein L.A., Uhrberg M., Parham P.;
 RT "Conservation and variation in human and common chimpanzee CD94 and


```
QY 130 FWVIGLRDIDG-WRWEDGPALSIILSNVVQ-----KCGTHRCG-LHASS 174
D 228 VSMVIGLTDQNGPWRWYDGTDFEKGFKNAPLQPDNWFHGHGGEDCAHITTGSPWNDDV 287
QY 175 CEVALQWICEKVL 187
D 288 CQTFRWICBMKL 300

RESULT 14
V239 FOWPV STANDARD; PRT; 163 AA.
AC F14371; Q9J500;
DT 01-JAN-1990 (Rel. 13, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Putative C-type lectin protein FPV239 (BamHI-ORF8).
GN FPV239.
OS Fowlpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OX NCBI_TaxID=10261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193820; PubMed=10729156;
RA Alfonso C.L., Tulman E.R., Lu Z., Zaak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus.";
RL J. Virol. 74:3815-3831(2000).
RN [2]
RP SEQUENCE OF 1-116 FROM N.A.
RC STRAIN=FP-9 / Isolate HP-438;
RX MEDLINE=88229622; PubMed=2836548;
RA Tomley F., Birns M., Campbell J., Boursnell M.E.G.;
RT "Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment
of fowlpox virus.";
RL J. Gen. Virol. 69:1025-1040(1988).
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
DR EMBL; AF198100; AAP44583.1; -.
DR EMBL; D00295; BAA0203.1; -.
DR PIR; H29963; WMVZF9.
DR HSSP; P05140; 2AFP.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Hypothetical protein; Lectin.
FT DOMAIN 48 159 C-TYPE LECTIN.
SQ SEQUENCE 163 AA; 18635 MW; 5156DC892885532 CRC64;

Query Match 14.98; Score 154; DB 1; Length 163;
Best Local Similarity 22.94; Pred. No. 3.7e-08;
Matches 38; Conservative 31; Mismatches 65; Indels 32; Gaps 5;

QY 33 PCVSYLWVALGILLTVILMS-----LLLYQRTLCGSGFMCSCSCPNIWMRNGS 84
D 18 PCGS--LIIVLSVFVILSTRPVPDPKILY-----CKEGWGVYKN 57
QY 85 HCYYFSMEKRDWNSLKFCAKDGSHLLTFPDNGVNLFOYVGVDFYWIGLRDID---GW 141
D :|||: : : : : : : : : : : : : : : : : : : : : : : : : : :
D 58 NCYFFSEKKNKSLAVERCKDMGHLTSISSKEBFKFLRYKGNHWIGIEKVDENGTV 117
QY 142 RWEDGPALSIILSNVVQKCGTHRCGLHASSCEVALQWICEKVL 187
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```
Db 118 KLEDSSYD-NIVPIKIGDCAYLSDRSINSMFCFLPKKWKRIIL 162
: |||: : : : : : : : : : : : : : : : : : : : : : : : : : :
: |||: : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
CD69 MOUSE STANDARD; PRT; 199 AA.
ID CD69_MOUSE
AC F37217;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Early activation antigen CD69.
GN CD69.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93314711; PubMed=8100776;
RA Ziegler S.F., Ramsdell F., Hjerrild K.A., Armitage R.J.,
RA Grabstein K.H., Hennen K.B., Farrah T., Fanslow W.C., Shevach E.M.,
RA Alderson M.R.;
RT "Molecular characterization of the early activation antigen CD69: a
type II membrane glycoprotein related to a family of natural killer
cell activation antigens.";
RL Eur. J. Immunol. 23:1643-1648(1993).
CC -!- FUNCTION: Involved in lymphocyte proliferation and functions as a
signal transmitting receptor in lymphocytes, natural killer (NK)
cells, and platelets.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T CELLS,
B-CELLS, NATURAL KILLER CELLS, NEUTROPHILS AND PLATELETS.
CC -!- DEVELOPMENTAL STAGE: Earliest inducible cell surface glycoprotein
acquired during lymphoid activation.
CC -!- INDUCTION: By the activation of T lymphocytes.
CC -!- PTM: CONSTITUTIVE SER/THR PHOSPHORYLATION IN BOTH MATURE
THYMOCYTES AND ACTIVATED T LYMPHOCYTES (BY SIMILARITY).
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L23638; -. NOT_ANNOTATED_CDS.
DR MGD; MGI:88343; CD69.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Antigen; Signal-anchor; Transmembrane; Lectin; Glycoprotein;
KW Phosphorylation.
FT DOMAIN 1 40 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 41 61 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 62 199 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 92 195 C-TYPE LECTIN.
FT DISULFID 68 85 BY SIMILARITY.
FT DISULFID 96 194 BY SIMILARITY.
FT DISULFID 173 186 BY SIMILARITY.
FT CARBOHYD 150 150 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 199 AA; 22517 MW; 39F8E4941D36D4F6 CRC64;
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Query Match 14.9%; Score 154; DB 1; Length 199;
Best Local Similarity 22.7%; Pred. NO. 4.6e-08;
Matches 35; Conservative 32; Mismatches 71; Indels 16; Gaps 4;

QY	45	LLTVILMSLLLYQRTLCGSKGFWC-----SQSRCPNLWMENGSHCHYFSMEK	93
Db	46	LIVVLITSLIITALINVGK--YNPCGLYEKLESSDHHVATCKNEWISYKRTCYFFSTTT	103
QY	94	RDWNSSLKFCADKGSLLITFPDNOGVNLFQYVGEDFYWIGLRD--IDGWREDGPALSL	151
Db	104	KSWALAQRSCEADATLAVIDSEKDMTFLKRYSGELEHWHIGLKNEANQTKWANGKEFN-	162
QY	152	SILNSVVQKCGTIHRCGLHASSCEVALQWICEK	185
Db	163	SWFNLTGSGRCVSVNHKNVTAVDCEANPHWVCSK	196

Search completed: August 10, 2004, 16:17:00
Job time : 7.32035 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:11:32 ; Search time 32.6089 Seconds
(without alignments)
1819.059 Million cell updates/sec

Title: US-09-811-367B-5
Perfect score: 1036
Sequence: 1 MADNSIYSLLEPAAPRVQD.....GLHASSCEVALQWICEKVLIP 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phase: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp Vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	11 Q64335	Q64335 rattus norv
2	838	80.9	188	11 Q88713	Q88713 mus musculus
3	545.5	52.7	189	4 Q75613	Q75613 homo sapien
4	541.5	52.3	195	4 Q96E93	Q96E93 homo sapien
5	525.5	50.7	189	4 Q43198	Q43198 homo sapien
6	201.5	19.4	275	11 Q9D403	Q9D403 mus musculus
7	184	17.8	257	13 Q90636	Q90636 gallus gall
8	178	17.2	181	4 Q9NZS1	Q9NZS1 homo sapien
9	178	17.2	231	4 Q9NZS2	Q9NZS2 homo sapien
10	177.5	17.1	200	13 Q802S8	Q802S8 gallus gall
11	177	17.1	231	6 Q8MI05	Q8MI05 macaca fasc
12	177	17.1	238	11 Q8BRU4	Q8BRU4 mus musculus
13	176.5	17.0	422	6 Q8HY11	Q8HY11 hylobates s
14	175	16.9	179	11 Q54708	Q54708 mus musculus
15	175	16.9	179	11 Q54707	Q54707 mus musculus
16	174.5	16.8	191	4 Q9UHP7	Q9UHP7 homo sapien

17	174.5	16.8	293	11 Q8CBB4	Q8CBB4 mus musculus
18	174.5	16.8	399	6 Q8HY12	Q8HY12 hylobates l
19	174.5	16.8	399	6 Q8HY10	Q8HY10 hylobates c
20	173.5	16.7	208	11 Q91ZW7	Q91ZW7 mus musculus
21	173	16.7	165	11 Q9R007	Q9R007 mus musculus
22	173	16.7	211	11 Q91ZW5	Q91ZW5 mus musculus
23	173	16.7	223	11 Q925G5	Q925G5 mus musculus
24	172	16.6	230	13 Q9PU48	Q9PU48 gallus gall
25	171	16.5	165	6 Q9GLF4	Q9GLF4 sus scrofa
26	170.5	16.5	227	11 Q91V25	Q91V25 mus musculus
27	170.5	16.5	227	11 Q61973	Q61973 mus musculus
28	170	16.4	223	11 Q925G3	Q925G3 mus musculus
29	169.5	16.4	225	4 Q12918	Q12918 homo sapien
30	169.5	16.4	233	6 Q8MJH7	Q8MJH7 pongo pygma
31	168.5	16.3	227	11 Q925G4	Q925G4 mus musculus
32	168.5	16.3	229	4 Q9P126	Q9P126 homo sapien
33	168.5	16.3	233	6 Q8MJH6	Q8MJH6 pongo pygma
34	168.5	16.3	237	11 Q91ZW8	Q91ZW8 mus musculus
35	167.5	16.2	200	6 Q8SPX1	Q8SPX1 sus scrofa
36	167.5	16.2	233	6 Q8MJ10	Q8MJ10 pongo pygma
37	167	16.1	217	11 Q64228	Q64228 mus sp. nkl
38	167	16.1	223	11 Q99P32	Q99P32 mus musculus
39	167	16.1	223	11 Q99JB4	Q99JB4 mus musculus
40	166	16.0	223	11 Q7TMP8	Q7TMP8 mus musculus
41	166	16.0	236	6 Q95L94	Q95L94 macaca mula
42	165.5	16.0	164	11 Q8BL24	Q8BL24 mus musculus
43	165.5	16.0	229	11 Q9JL99	Q9JL99 mus musculus
44	165.5	16.0	233	6 Q8MJH8	Q8MJH8 pongo pygma
45	165.5	16.0	376	6 Q8HY06	Q8HY06 gorilla gor

ALIGNMENTS

RESULT 1

ID Q64335 PRELIMINARY; PRT; 188 AA.
AC Q64335;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MAFa protein.
GN MAFa.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=Testis;
RA Bocek Jr P., Gutmann M.D., Pecht I.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96016176; PubMed=7568140;
RA Gutmann M.D., Tal M., Pecht I.;
RT "A secretion inhibitory signal transduction molecule on mast cells is another C-type lectin."
RL Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).
DR EMBL; X97191; CAA65829.1; -.
DR EMBL; X97192; CAA65829.1; JOINED.
DR EMBL; X97193; CAA65829.1; JOINED.
DR EMBL; X97194; CAA65829.1; JOINED.
DR EMBL; X97195; CAA65829.1; JOINED.
DR EMBL; X79812; CAA56208.1; -.
DR PIR; I59421; I59421.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF000059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
SQ SEQUENCE 188 AA; 21355 MW; 2CC9032D4D020B15 CRC64;

Query Match 100.0%; Score 1036; DB 11; Length 188;
 Best Local Similarity 100.0%; Pred. No. 1e-102;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRCPCVSYLVMAVALGLTTLVILMSLLLYQRTL 60
 DB 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRCPCVSYLVMAVALGLTTLVILMSLLLYQRTL 60

QY 61 CCGSGKGFMCSCSRCPNLWMRNGSHCYFFSMKRDWNSLKFCADKSGHLLTFFPDNQGVN 120
 DB 61 CCGSGKGFMCSCSRCPNLWMRNGSHCYFFSMKRDWNSLKFCADKSGHLLTFFPDNQGVN 120

QY 121 LFOEYVGEDFWIGLRIDGWRWEDGPAISLSILSNSVVKCGTTHRCGLHASSCEVALQ 180
 DB 121 LFOEYVGEDFWIGLRIDGWRWEDGPAISLSILSNSVVKCGTTHRCGLHASSCEVALQ 180

QY 181 WICEKVL 188
 DB 181 WICEKVL 188

RESULT 2

O88713 PRELIMINARY; PRT; 188 AA.

ID O88713
 AC O88713;
 DT 01-NOV-1998 (TREMELrel. 08, Created)
 DT 01-AUG-1999 (TREMELrel. 11, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-like receptor G1).
 DE Like receptor G1.
 GN KLRG1 OR MAFA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C.B-17 SCID;
 RX MEDLINE=99077194; PubMed=9862378;
 RA Hanke T., Corral L., Vance R.E., Raullet D.H.;
 RT "2F1 antigen, the mouse homolog of the rat '31', is a lectin-like type II transmembrane receptor expressed by natural killer cells.";
 RL Eur. J. Immunol. 28:4409-4417(1998).
 RN [2]
 RP SEQUENCE OF 2-188 FROM N.A.
 RA Blaser C.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvevTACfBr; TISSUE=Spleen;
 RX MEDLINE=21115136; PubMed=11220622;
 RA Voehringer D., Kaufmann M., Bircher H.;
 RT "Genomic structure, alternative splicing, and physical mapping of the killer cell lectin-like receptor G1 gene (KLRG1), the mouse homologue of MAFA.";
 RL Immunogenetics 52:206-211(2001).
 DR EMBL; AF097357; AAD03718.1; -;
 DR EMBL; AJ010751; CAA09342.1; -;
 DR EMBL; AF317727; AAK40082.1; -;
 DR MGB; MGI:1355294; Klrkl.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
 KW Lectin; Receptor.
 SQ SEQUENCE 188 AA; 21396 MW; 876336802EAL34F1 CRC64;

Query Match 80.9%; Score 838; DB 11; Length 188;
 Best Local Similarity 80.7%; Pred. No. 1.6e-81;
 Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRCPCVSYLVMAVALGLTTLVILMSLLLYQRTL 60
 DB 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRCPCVSYLVMAVALGLTTLVILMSLLLYQRTL 60

QY 61 CCGSGKGFMCSCSRCPNLWMRNGSHCYFFSMKRDWNSLKFCADKSGHLLTFFPDNQGVN 120
 DB 61 CCGSKDSTCSCHPCPILWTGSHCYFFSMKRDWNSLKFCADKSGHLLTFFPDNQGVK 120

QY 121 LFOEYVGEDFWIGLRIDGWRWEDGPAISLSILSNSVVKCGTTHRCGLHASSCEVALQ 180
 DB 121 LFEYLGDFWIGLRIDGWRWEGGPALSRLITNSLIQRCGAIHRNGLOASSCEVALQ 180

QY 181 WICEKVL 187
 DB 181 WICKKVL 187

RESULT 3
 O75613 PRELIMINARY; PRT; 189 AA.

ID O75613
 AC O75613;
 DT 01-NOV-1998 (TREMELrel. 08, Created)
 DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE ITIM-containing receptor MAFA-L.
 GN MAFA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Butcher S., Arney K.L., Cook G.P.;
 RT "MAFA-L, an ITIM-containing receptor encoded by the human NK cell gene complex and expressed by basophils and NK cells.";
 RL Eur. J. Immunol. 28:0-0(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99077194; PubMed=9862378;
 RA Hanke T., Corral L., Vance R.E., Raullet D.H.;
 RT "2F1 antigen, the mouse homolog of the rat '31', is a lectin-like type II transmembrane receptor expressed by natural killer cells.";
 RL Eur. J. Immunol. 28:4409-4417(1998).
 DR EMBL; AF081675; AAC32200.1; -;
 DR EMBL; AF097358; AAD03719.1; -;
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
 SQ SEQUENCE 189 AA; 21206 MW; FA9023F1523656A8 CRC64;

Query Match 52.7%; Score 545.5; DB 4; Length 189;
 Best Local Similarity 55.1%; Pred. No. 3.1e-50;
 Matches 103; Conservative 28; Mismatches 55; Indels 1; Gaps 1;

QY 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRCPCVSYLVMAVALGLTTLVILMSLLLYQRTL 60
 DB 1 MTDSVIYSMLLELPTATQNDYGPQKSSSRPSCCLVALGLTAVLLSVLLYQWIL 60

QY 61 CCGSGKGFMCSCSRCPNLWMRNGSHCYFFSMKRDWNSLKFCADKSGHLLTFFPDNQGVN 120
 DB 61 CCGSNYSTCASCPCPDPRWKMVGNHCYFFSVEKDWNSSLFCLARDSHLLVITDQEMS 120

QY 121 LFOEYVGEDFWIGLRIDGWRWEDGPAISLSILSNSVVKCGTTHRCGLHASSCEVALQ 179
 DB 121 LLQVFLSEAFWIGLRNNSGWRWEDGSPINFSRISNSFVQTCGAINKNGLOASSCEVPL 180

QY 180 QWICEKV 186
 DB 181 HWCKKV 187


```

RESULT 4
Q96E93 ID Q96E93 PRELIMINARY; PRT; 195 AA.
AC Q96E93;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to killer cell lectin-like receptor subfamily G, member 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012621; AAH12621.1; -.
DR Genew; HGNC:6380; KLRG1.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PSS0041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Receptor.
SQ SEQUENCE 195 AA; 21831 MW; 178E98B08EBC473 CRC64;

Query Match 52.3%; Score 541.5; DB 4; Length 195;
Best Local Similarity 54.8%; Pred. No. 8.6e-50;
Matches 102; Conservative 28; Mismatches 55; Indels 1; Gaps 1;

QY 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRCVSYLVNVALGLLTAVILMSLLYQRTL 60
Db 1 MTDSVIYSMLELPTATQAQNDYGPQOKSSSSKSCCLVAIGLLTAVLLSVLLYQWIL 60

QY 61 CCGSKGFMCSQCRCPNLWNRNGSHCYFFSMKRDWNSLKPCADKSGHLLTPPDNGVN 120
Db 61 CCGSNYSTCASCPCPDPRWKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120

QY 121 LFOEYVGEDFYWIGLRIDGWRWEDGPAISLS-ILNSVVKCGTTHRCGLHASSCEVAL 179
Db 121 LLQVFUSEAFCWIGLRNNSGWRWEDGSPFNFSRISSNSFVQTCGAINKNGQLASSCEVPL 180

QY 180 QWICEK 185
Db 181 HWCKK 186

Query Match 50.7%; Score 525.5; DB 4; Length 189;
Best Local Similarity 53.5%; Pred. No. 4.3e-48;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRCVSYLVNVALGLLTAVILMSLLYQRTL 60
Db 1 MTDSVIYSMLELPTATQAQNDYGPQOKSSSSKSCCLVAIGLLTAVLLSVLLYQWIL 60

QY 61 CCGSKGFMCSQCRCPNLWNRNGSHCYFFSMKRDWNSLKPCADKSGHLLTPPDNGVN 120
Db 61 CCGSNYSTCASCPCPDPRWKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120

QY 121 LFOEYVGEDFYWIGLRIDGWRWEDGPAISLS-ILNSVVKCGTTHRCGLHASSCEVAL 179
Db 121 LLQVFUSEAFCWIGLRNNSGWRWEDGSPFNFSRISSNSFVQTCGAINKNGQLASSCEVPL 180

QY 180 QWICEK 186
Db 181 HWCKK 187

RESULT 6
Q9D403 ID Q9D403 PRELIMINARY; PRT; 275 AA.
AC Q9D403;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 4933425B16RIK protein.
GN 4933425B16RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK016908; BAB30491.1; -.
DR HSP; P23807; IXX.

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DR MGD; MGI:1918433; 4933425B16rik.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C.TYPE LECTIN_2; 1.
SQ SEQUENCE 275 AA; 31360 MW; C9792BA25C8B5CC2 CRC64;

Query Match 19.4%; Score 201.5; DB 11; Length 275;
Best Local Similarity 23.4%; Pred. No. 3.1e-13;
Matches 63; Conservative 40; Mismatches 77; Indels 89; Gaps 11;

QY 1 MADNSIYSTLELPAAPRVQ-----DDSRWKVAVLHRCVSVYLVNVALGL 45
DB 1 MSDEVYATMLQDSARVGRNDRGNLRKEGHPAQSSLWRGAAL---SLMILCIVLVTL 57
QY 46 LTVILM-----SLLLY 56
DB 58 VTLATMFLQVNSDINSDEKLSQLQKSIHPQODNLSELSRSKSLTEBSLQSQISALLE 117
QY 57 QR-----TLCGSGKPMC-----SQSCRCPNLMWRNGSHCYFESM-EKRDWNSLKECADKG 107
DB 118 ROEQMATKLC--KEFLIHADHKCNPCPTWQYNGNSCYFYSINEEKSWSDSRDCIDKN 175
QY 108 SHLLTFPDNQGVNLFQEVVG--EDFYWIGLR-DIDG--WRWEDGFPALSLILNSVW--- 159
DB 176 ATLKVIDSTERDLQLSQLSTFFFWLGLSNSSGRNWLWEDGSPFPPTLLSDKELASF 235
QY 160 ---OKGTHRCGLHASCEVALQWICEK 185
DB 236 NGSRECAYPFERGNIYVTSRAEIPWICEK 264

RESULT 7
Q90636 PRELIMINARY; PRT; 257 AA.
AC Q90636;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 17.5 protein.
GN 17.5.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=94164691; PubMed=8119728;
RA Bernot A., Zoorob R., Auffray C.;
RT "Linkage of a new member of the lectin supergene family to the chicken
RT Mhc genes.";
RL Immunogenetics 39:221-229(1994).
DR EMBL; M8072; AAA48558.1; --
DR PIR; I50146; I50146.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C.TYPE LECTIN_2; 1.
SQ SEQUENCE 257 AA; 28814 MW; C67EA483F4E85333 CRC64;

Query Match 17.8%; Score 184; DB 13; Length 257;
Best Local Similarity 28.6%; Pred. No. 2.2e-11;
Matches 46; Conservative 23; Mismatches 66; Indels 26; Gaps 6;

QY 33 PCVSYLVNVALGLTIVILMLLLVORTLCCGSKGPMCSQSCRCPNLMWRNGSHCYFESME 92
DB 101 PC-----MLVALVAVIL-----QRPCSPRPFF-----SHVCPNAWVGFQCKYFTSDT 146

us-09-811-367b-5.open.rspt

QY 93 KRDWNSLKECADKGSLLTFPDNQGVNLFQEVVGEDFYWIGLRDIDG---WRWEDGFPAL 149
DB 147 ESDWNSREHCHRLGASLATLDTKEEMFELQYQRPADRWTLGLHRAEGDEHWTWADGSF 206
QY 150 SLILNSVWQ-----KCGTHRCGLHASCEVALQWICEK 185
DB 207 T-----NRPVFLRGGRCAYLNGDGISSALCHSEKFWVCSR 243

RESULT 8
Q9NZS1 PRELIMINARY; PRT; 181 AA.
AC Q9NZS1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lectin-like receptor F1, splice variant 1 KLRFL-sl.
GN KLRFL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20135860; PubMed=10671213;
RA Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
RA Fernandez-Ruiz E.;
RT "Human KLRFL, a novel member of the killer cell lectin-like receptor
RT gene family: molecular characterization, genomic structure, physical
RT mapping to the NK gene complex and expression analysis.";
RL Eur. J. Immunol. 30:568-576(2000).
DR EMBL; AF175207; AAF37805.1; --
DR GO; GO:0016020; C:membrane; TAS.
DR GO; GO:0030106; F:MHC class I receptor activity; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C.TYPE LECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 181 AA; 21204 MW; 64642240CAEIE551 CRC64;

Query Match 17.2%; Score 178; DB 4; Length 181;
Best Local Similarity 25.0%; Pred. No. 6.2e-11;
Matches 51; Conservative 32; Mismatches 77; Indels 44; Gaps 9;

QY 1 MADNSIYSTLELPAAPRVQ-DDSRWKVYK---AVLHRCVSVYLVNVAL-----GLITVILM 51
DB 1 MQDEERYMTLNVQSKRASSAQTSQITFKDYSVTLH---WYKILLGISGTVNGILTLI 56
QY 52 SLLLYQRTLCGSKGPMCSQSCRCPNLMWRNGSHCYFESMEKRDWNSLKECADKGSLL 111
DB 57 SLIL-----LVLQSEWLKYQCKYFNSNEMKWSDSVYVYCLERKSHL 100
QY 112 TFPDNQGVNLFQEVVG--DFYWIGLRDIDG---GWRWEDGFPALSLIL-----SNSVWQ 160
DB 101 IHHOLEMAFIQKNLRQINLVNIGLNTSLKMTWTWVDGSPIDSKIFIKGPAKENS---- 157
QY 161 KCGTHRCGLHASCEVALQWICE 184
DB 158 -CAAIKESKIFSETCSSVFKWICQ 180

RESULT 9
Q9NZS2 PRELIMINARY; PRT; 231 AA.
AC Q9NZS2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lectin-like receptor F1 (Activating coreceptor NKp80).
GN KLRFL OR ML/KLRFL.
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN NCBI_TaxID=9606;
[1]
RX MEDLINE=20135860; PubMed=10671213;
RA Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
RA Fernandez-Ruiz E.;
RT "Human KIR2F, a novel member of the killer cell lectin-like receptor
RT gene family: molecular characterization, genomic structure, physical
RT mapping to the NK gene complex and expression analysis.";
RL Eur. J. Immunol. 30:568-576(2000).
RN [2]
RP SEQUENCE FROM N.A.
KC TISSUE=Lymphoid;
RX MEDLINE=21150889; PubMed=11265639;
RA Vitale M., Falco M., Castriiconi R., Parolini S., Zambello R.,
RA Semenzato G., Biassoni R., Bottino C., Moretta L., Moretta A.;
RT "Identification of NKp80, a novel triggering molecule expressed by
RT human natural killer cells.";
RL Eur. J. Immunol. 31:233-242(2001).
DR EMBL; AF175206; AAF37804.1; -.
DR EMBL; AJ305370; CAC29425.1; -.
DR Genbank; HGNC:13342; KIR2F.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
DR GO; GO:0006166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin.c; 1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 231 AA; 26562 MW; A2F7BE6D4341AFDE CRC64;

Query Match 17.2%; Score 178; DB 4; Length 231;
Best Local Similarity 23.3%; Pred. No. 8.3e-11;
Matches 56; Conservative 34; Mismatches 84; Indels 66; Gaps 11;

QY 1 MADNSYSTLELPAAPRVQ-DDSRWKVK----AVLHRCVSYLVNVAL-----GLLTIVLM 51
DB 1 MQDEERYMTLVNQSKRSSAQTSQTLTKDYSVTLH----WKILLGSGTVNGILTLTI 56

QY 52 SLLLY-----QRTLC-----CGSKGFCWSCQSCR 75
DB 57 SLLLYSQVLLKQKQSCSNATQYEDTGLKVNNGTRRNISNKDLCASRS--ADQTVLC 114

QY 76 PNLWMRNGSHCYFYSMEKRDWNSLKFCDKSGHLLTFPPNQGNLFOEYVVG-DFYVIG 134
DB 115 QSEWLKYGQCYWFNSMKSWSDSYVYCLERKSHLLIHLHOLEMAFLQKNLRQINLVYVIG 174

QY 135 LRID---GMRWEDGPALSIL-----SNSVVKCGTHRCGLHASSCEVALOWICE 184
DB 175 LNFETSLKMTWTWVDGSPIDSKIFFKIPKPAKENS-----CAAIKESKIPSETCSSVFKWICQ 230

RESULT 10
ID Q80258 PRELIMINARY; PRT; 200 AA.
AC Q80258;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C-type lectin.
GN Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Rogers S., Shaw I., Ross N., Nair V., Rothwell L., Kaufman J.,

RA Kaiser P.;
RT "Analysis of part of the chicken Rfp-Y region reveals two novel lectin
RT genes, the first complete genomic sequence of a class I alpha-chain
RT gene, a truncated class II beta-chain gene, and a large CRI repeat.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277927; CAD61336.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin.c; 1.
DR PRINTS; PR00356; ANTI-FREZEII.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin.
SQ SEQUENCE 200 AA; 22573 MW; 23AA950D11334988 CRC64;

Query Match 17.1%; Score 177.5; DB 13; Length 200;
Best Local Similarity 26.1%; Pred. No. 7.9e-11;
Matches 42; Conservative 24; Mismatches 66; Indels 29; Gaps 5;

QY 39 VMVALGLLTIVLMSLLLYQRTLCCKSGKFCWSCQ-----CSRCPLNLMRNGSHCYF 89
DB 41 VCAALGALLILVLVI-----STVCRQVPVPPFPDFAHACPNAAWVGQKCYF 88

QY 90 SMEKRDWNSLKFCDKSGHLLTFPPNQGNLFOEYVVGDFYVIGL---RDIDGWRWEDG 146
DB 89 SKEENDWNSRHCNAHGASLATIGSAEEMFMRFQGPANCWIGLHREEDAQWTWSDG 148

QY 147 PALS---LSILSNSVVKCGTHRCGLHASSCEVALOWICEK 185
DB 149 TAFTNWFEIRGGG---RCAYLNGDRISSLSLCHLKHVWCSR 186

RESULT 11
ID Q8MI05 PRELIMINARY; PRT; 231 AA.
AC Q8MI05;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NKp80 NK receptor.
GN NKp80.
OC Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
KC TISSUE=NK lymphocytes;
RA Biassoni R.;
RT "Macaca fascicularis NK cell and receptors.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ426430; CAD19994.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin.c; 1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 231 AA; 26710 MW; 403C79CA68893C1E7 CRC64;

Query Match 17.1%; Score 177; DB 6; Length 231;
Best Local Similarity 23.5%; Pred. No. 1.1e-10;
Matches 56; Conservative 32; Mismatches 88; Indels 62; Gaps 10;

QY 1 MADNSYSTLELPAAPRVQDDSRW----KVAVLHRCVSYLVNVAL-----GLLTIVLM 51
DB 1 MQDEERYMTLVNQSKKRTSTQTLTKDYSVVLH----WKILLGSGTLGILALALI 56

QY 52 SLLLY---QRTLCCKSGKF-----MC-----SQCSRCPN 77

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Db 57 SLILVSGVLLKCKGSHNSHTTETDGLKMNNGTERTNSKDLVSRADQTVLCQS 116
QY 78 LWMRNGSHCYFVSFMEKRDWNSLKFCADKGGSHLLTFPPNQGNVLFQEVYGEDFY-WIGLR 136
Db 117 EWLKYGKCYWFSNEMKSWSDSYVYCLERKSHLLIODELEMAFTQKNLQSNYVWMLN 176
QY 137 DID---GWRWEDGPALSLSL-----SNSVVKCGTIHRCGLHASCEVALQWICE 184
Db 177 FTSLKMTWTWVDGSLDPKIFIKGPAKENS-----CAAIKSKIYSETCSSVFKWICQ 230

RESULT 12
Q8BRU4 PRELIMINARY; PRT; 238 AA.
AC Q8BRU4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical C-type lectin domain containing protein.
GN 9830005G06RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta, and Vein;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK041288; BAC30890.1; -.
DR MGD; MGI:2444608; 9830005G06RIK.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; AntifreezeZell.
DR Pfam; PF00059; Lectin_C_1.
DR PRINTS; PR00356; ANTI-FREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 27014 MW; 07368A0380B95EAL CRC64;

Query Match 17.1%; Score 177; DB 11; Length 238;
Best Local Similarity 25.7%; Pred. No. 1.1e-10;
Matches 63; Conservative 30; Mismatches 78; Indels 74; Gaps 12;

QY 1 MADNSIYSTL--ELP---AAPRVQDSR-----WKVKAVLHRCPCVSYLVWVALGILL-TVIL 50
Db 1 MHAEEIYTSIQWDIPTSEASOKSPSKGAWCVVTMI--SCV-----VCMGLLAYSIF 53
QY 51 MSL-----LQYRTLCGSKGFMCSQ 71
Db 54 LGIKFFQVSSVLVQERLIQDITALVNLQWQRYTLEYCQALLQSLHSG-----SD 107
QY 72 CSRCPNLWMRNGSHCYFVSFMEKRDWNSLKFCADKGGSHLLTFPPNQGNVLFQ---EYVGE 128
Db 108 CSPCPHNWQNGKSCYVFERWENWNISKKSLCEGASLFQDSKEEMEFISITGLKGG 167
QY 129 DFYWIGLRDIDG---NRWEDGPALSLSL-----SNSVVKCGTIHRCGLHASCEVALQ 180
Db 168 NKYVWGVFQ-DGISGSFWEDGSSPLSDLLPAERQSRAGQCYGLKSDTLISDKDSWKY 226
QY 181 WICEK 185
Db 227 FICEK 231
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RESULT 13

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Q8HY11 PRELIMINARY; PRT; 422 AA.
AC Q8HY11;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative CD209L1 protein.
GN CD209L1.
OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B1533;
RX PubMed=12477827;
RA Bashirova A.A.; Wu L.; Cheng J.; Martin T.D.; Martin M.P.;
RA Benveniste R.E.; Lifson J.D.; Kewallamani V.N.; Hughes A.;
RA Carrington M.;
RT "Novel Member of the CD209 (DC-SIGN) Gene Family in Primates.";
RL J. Virol. 77:217-227 (2003).
DR EMBL; AY078820; AAL89529.1; -.
DR EMBL; AY078814; AAL89529.1; JOINED.
DR EMBL; AY078815; AAL89529.1; JOINED.
DR EMBL; AY078816; AAL89529.1; JOINED.
DR EMBL; AY078817; AAL89529.1; JOINED.
DR EMBL; AY078818; AAL89529.1; JOINED.
DR EMBL; AY078819; AAL89529.1; JOINED.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; AntifreezeZell.
DR InterPro; IPR001304; Lectin_C_1.
DR Pfam; PF00059; Lectin_C_1.
DR PRINTS; PR00356; ANTI-FREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 422 AA; 48031 MW; 1F24460CBF991DC3 CRC64;

Query Match 17.0%; Score 176.5; DB 6; Length 422;
Best Local Similarity 29.9%; Pred. No. 2.5e-10;
Matches 38; Conservative 19; Mismatches 57; Indels 13; Gaps 3;

QY 72 CSRCPNLWMRNGSHCYFVSFMEKRDWNSLKFCADKGGSHLLTFPPNQGNVLFQEVYGED-- 129
Db 288 CCRCPKDWTTFQGNCYFMSNSQRNWHDSVTACQEVAGLVVKSAEQNFLOQTSRNR 347
QY 130 FYWIGLRDID---GWRWEDGPALSLSL-----SNSVVKCGTIHRCGLHASCEVA 178
Db 348 FSWMGLSDLAQEGTWQVDGSPLSLSSSFQRYWNSGEPNNSGDECAEFSGSGMNDRCNVD 407
QY 179 LOWICEK 185
Db 408 NYWICKK 414

RESULT 14
Q54708 PRELIMINARY; PRT; 179 AA.
AC Q54708;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD94.
GN KLRI1 OR CD94.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CB.17 SCID;
RX MEDLINE=98124458; PubMed=9464811;
RA Vance R.E.; Tanamachi D.M.; Hanke T.; Raullet D.H.;
```

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RT "Cloning of a mouse homolog of CD94 extends the family of C-type
RT lectins on murine natural killer cells.;"
RL Eur. J. Immunol. 27:3236-3241(1997).
DR EMBL; AF030312; AAC28244.1; -.
DR MGD; MGI:1196275; Klrd1.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF like.
DR DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C TYPE LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
SQ SEQUENCE 179 AA; 20809 MW; D59ELCB63139B45 CRC64;

Query Match 16.9%; Score 175; DB 11; Length 179;
Best Local Similarity 27.9%; Pred. No. 1.3e-10;
Matches 50; Conservative 36; Mismatches 71; Indels 22; Gaps 10;

QY 22 SRWKVAVLHR-PCVSYLVNVALGLLTIVILMSLLLYQRTLC-CGSKGFM-CSQCSRCPNL 78
Db :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
7 TRWRLMSVIFGIKCL--FLMVTILGVLLINSFTIQSTPSTTTVEFQEVSECCVCLDK 64

QY 79 WMENGSHCYFYSMEKRDWNSLKFCADKSGSHLLTFPDNOGVNLFQEVYVGEDFYWIGL--- 135
Db :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
65 WVGHCNCYFISKEKSWERSRDFCASQNSLLQ-PQSRNELSFMNF-SQTFFWIGMHYS 122

QY 136 RDIDGHRWEDGPALSILSN-SVQKCGTIHRC-----GLHASSCEVALOWICEKV 186
Db :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
123 EKENAMLWEDGTVPKDLFPFVSIRP---EHCIVVSPSKSVSAESCENKRYICKL 177

Search completed: August 10, 2004, 16:18:50
Job time : 33.6089 secs

RESULT 15
O54707 PRELIMINARY; PRT; 179 AA.
AC O54707;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Killer cell lectin-like receptor, subfamily D, member 1 (CD94).
GN KLRD1 OR CD94.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Vance R.B., Tanamachi D.M., Hanke T., Raullet D.H.;
RL Eur. J. Immunol. 27:0-0(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Heusel J.W., Ho E.I., Brown M.G., Matsumoto K., Yokoyama W.M.;
RL "Murine CD94.;"
RN Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Butcher S., Cottage A., Cook G.P.;
RL "Mouse natural killer cell receptors homologous to human CD94 and
RT NKG2-D.;"
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF030311; AAC28243.1; -.
DR EMBL; AF057714; AAC33713.1; -.
DR EMBL; AF039025; AAD02116.1; -.
DR MGD; MGI:1196275; Klrd1.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:05:01 ; Search time 46.5841 Seconds
(without alignments)
1140.281 Million cell updates/sec

Title: US-09-811-367b-5

Perfect score: 1036

Sequence: 1 MADNSIYSTLELPAPRVQD.....GLHSSCEVALQWICEKVLV 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1036	100.0	188	2 AAR77033	Mammalian
2	1036	100.0	188	2 AAW88277	Rat mast
3	1036	100.0	188	4 AAE11761	Rat mast
4	838	80.9	188	4 AAE11760	Mouse mas
5	651	62.8	114	2 AAR77472	Partial s
6	545.5	52.7	189	7 ADD25635	Binding d
7	525.5	50.7	189	2 AAW88265	Human mas
8	525.5	50.7	189	4 AAE11759	Human mas
9	418.5	40.4	843	4 ABG05451	Novel hum
10	251.5	24.3	191	6 ABJ37898	NOVX prot
11	207.5	20.0	99	2 AAW88267	Human MAF
12	184.5	17.8	199	2 AAR54659	Human CD6
13	184.5	17.8	199	2 AAW85593	Human CD6
14	184.5	17.8	199	7 ADD25621	Binding d
15	184	17.8	227	2 AAW85594	Chicken 1
16	183	17.7	228	4 AAU02495	Human sec
17	182	17.6	268	6 ABJ19328	NOVX rela
18	182	17.6	276	6 ABR43190	Human REM
19	182	17.6	276	6 AAE37769	Human C-t
20	180	17.4	231	5 ABB81897	Human Nkp
21	179.5	17.3	241	7 ADE07884	Novel pro
22	179.5	17.3	265	5 AAU19657	Human nov
23	179.5	17.3	265	5 ABP47877	Human pol
24	179.5	17.3	265	7 ADC10839	Human ext
25	179.5	17.3	275	6 ABJ19327	NOVX rela

ALIGNMENTS

RESULT 1

AAR77033
ID AAR77033 standard; protein; 188 AA.

XX AAR77033;

DT 01-FEB-1996 (first entry)

XX Mammalian mast cell function-associated antigen (MAFA).

KW Mast cell function-associated antigen; MAFA; soluble; ligand;
KW identification; screening; inflammation; inflammatory; allergy; allergic;
KW prevention.

OS Rattus rattus.

PN WO9527734-A1.

XX 19-OCT-1995.

PF 06-APR-1995; 95WO-US004258.

XX 08-APR-1994; 94IL-00109257.

XX (YEDA) YEDA RES & DEV CO LTD.
XX (RYCU//) RYCUS A.

XX Pecht I, Guthmann MD, Tal M;

XX WPI; 1995-366356/47.

XX N-PSDB; AAT01471.

XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -
XX useful for screening for ligands of MAFA which are useful for prevention
XX of inflammatory and allergic reactions.

XX Claim 12; Page 37; 54pp; English.

XX A soluble form of mast cell function-associated antigen (MAFA) can be
XX produced by recombinant techniques for use in the ligand- screening
XX assay. The ligands that are identified may be used alone or in
XX combination with the MAFA to prevent inflammatory and allergic reactions

SQ Sequence 188 AA;

Query Match 100.0%; Score 1036; DB 2; Length 188;

Best Local Similarity 100.0%; Pred. No. 1.8e-96;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Abr43189 Human REM
Aay66765 Membrane-
Aau1432 Human PRO
Aab65288 Human PRO
Abp43587 Membrane
Abu59103 Human PRO
Abu59181 Novel hum
Abu82693 Human sec
Abo17876 Novel hum
Abu60612 Human sec
Abu13994 Human PRO
Abu81130 Human PRO
Abu72579 Novel hum
Abu66830 Human PRO
Abr39424 Human GEN
Abu59911 Novel sec
Abu59328 Human sec
Abo26025 Human PRO
Abo25101 Human sec
Abu59034 Human sec

26 179.5 17.3 295 6 ABR43189
27 177.5 17.1 229 3 AAY66765
28 177.5 17.1 229 4 AAU1432
29 177.5 17.1 229 4 AAB65288
30 177.5 17.1 229 5 ABP43587
31 177.5 17.1 229 6 ABUS8103
32 177.5 17.1 229 6 ABUS9181
33 177.5 17.1 229 6 ABUS2693
34 177.5 17.1 229 6 ABO17876
35 177.5 17.1 229 6 ABUS60612
36 177.5 17.1 229 6 ABUI3994
37 177.5 17.1 229 6 ABUS81130
38 177.5 17.1 229 6 ABU72579
39 177.5 17.1 229 6 ABUS66830
40 177.5 17.1 229 6 ABR39424
41 177.5 17.1 229 6 ABUS9911
42 177.5 17.1 229 6 ABUS9328
43 177.5 17.1 229 6 ABO26025
44 177.5 17.1 229 6 ABO25101
45 177.5 17.1 229 6 ABUS9034

QY 1 MADNSIYGTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMMVALGLLTVILMSLLLYQRTL 60
 DB 1 MADNSIYGTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMMVALGLLTVILMSLLLYQRTL 60
 QY 61 CCGSGKGFMCSCQCRPNLWMRNGSHCYFFSMKRDWNSLKFCDKDGSHLLTFPDPNQGVN 120
 DB 61 CCGSGKGFMCSCQCRPNLWMRNGSHCYFFSMKRDWNSLKFCDKDGSHLLTFPDPNQGVN 120
 QY 121 LFOEYVVGDFYWGILRDIDGWRWEDGPALSLSILSNSVVKCGTTHRCGLHASSCEVALQ 180
 DB 121 LFOEYVVGDFYWGILRDIDGWRWEDGPALSLSILSNSVVKCGTTHRCGLHASSCEVALQ 180
 QY 181 WICEKVLVP 188
 DB 181 WICEKVLVP 188
 RESULT 2
 AAW88277
 ID AAW88277 standard; protein; 188 AA.
 AC AAW88277;
 DT 29-MAR-1999 (first entry)
 DE Rat mast cell function-associated antigen (MAFA).
 KW Mast cell function-associated antigen; MAFA; splice variant; rat;
 KW inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
 OS Rattus sp.
 FH Key Location/Qualifiers
 FT Modified-site 82..84
 FT Modified-site /note= "Asn is N-glycosylated"
 FT Modified-site 97..99
 FT Modified-site /note= "Asn is N-glycosylated"
 PN WO9854209-A2.
 XX
 PD 03-DEC-1998.
 XX
 PF 29-MAY-1998; 98WO-GB001572.
 XX
 PR 31-MAY-1997; 97GB-00011148.
 XX
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
 XX
 PI Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
 XX WPI; 1999-059806/05.
 DR N-PSDB; AAV84222.
 XX
 PT New polypeptide having a sequence corresponding to human mast cell
 PT function-associated antigen - useful in forming and manufacturing
 PT pharmaceutical compositions in the treatment of inflammatory and allergic
 PT diseases, and tumour growth.
 XX
 PS Disclosure; Fig 4; 44pp; English.
 XX
 CC This is the amino acid sequence of rat mast cell function-associated
 CC antigen (MAFA), a type II membrane glycoprotein found on mast cells and
 CC basophils. The invention relates to cloning of the human MAFA molecule
 CC (see AAW88265) and to the discovery of splice variants (see AAW88266-67)
 CC of human MAFA that are not found in rat. Polypeptides and synthetic
 CC peptides (see AAW88258-64) based on human MAFA and human truncated MAFA,
 CC and polynucleotides encoding them, can be used in methods for the
 CC treatment of inflammatory and allergic diseases (e.g. rheumatoid
 CC arthritis and asthma), and tumour growth
 XX
 SQ Sequence 188 AA;

Query Match 100.0%; Score 1036; DB 2; Length 188;
 Best Local Similarity 100.0%; Pred. No. 1.8e-96;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MADNSIYGTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMMVALGLLTVILMSLLLYQRTL 60
 DB 1 MADNSIYGTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMMVALGLLTVILMSLLLYQRTL 60
 QY 61 CCGSGKGFMCSCQCRPNLWMRNGSHCYFFSMKRDWNSLKFCDKDGSHLLTFPDPNQGVN 120
 DB 61 CCGSGKGFMCSCQCRPNLWMRNGSHCYFFSMKRDWNSLKFCDKDGSHLLTFPDPNQGVN 120
 QY 121 LFOEYVVGDFYWGILRDIDGWRWEDGPALSLSILSNSVVKCGTTHRCGLHASSCEVALQ 180
 DB 121 LFOEYVVGDFYWGILRDIDGWRWEDGPALSLSILSNSVVKCGTTHRCGLHASSCEVALQ 180
 QY 181 WICEKVLVP 188
 DB 181 WICEKVLVP 188
 RESULT 3
 AAE11761
 ID AAE11761 standard; protein; 188 AA.
 AC AAE11761;
 DT 18-DEC-2001 (first entry)
 DE Rat mast cell function associated antigen (MAFA) protein.
 KW Rat; pharmaceutical composition; mast cell function associated antigen;
 KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
 KW immunosuppressive; cytostatic.
 OS Rattus norvegicus.
 XX WO200170805-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 16-MAR-2001; 2001WO-US008596.
 XX
 PR 17-MAR-2000; 2000US-0190716P.
 XX
 PA (GEMI-) GEMINI SCI INC.
 XX
 PI Takahashi N, Mikayama T;
 XX WPI; 2001-611482/70.
 DR N-PSDB; AAD18736.
 XX
 PT Pharmaceutical composition for treating tumor by stimulating cytotoxic
 PT activity of natural killer cell or T-cell, comprises an agent that binds
 PT to mast cell function-associated antigen ligand on target cell.
 PS Example 1; Page 19; 49pp; English.
 XX
 CC The present invention relates to a pharmaceutical composition comprising
 CC an agent which specifically binds to a mast cell function associated
 CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
 CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
 CC ligand and a pharmaceutically acceptable excipient. The invention is
 CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
 CC binding to a ligand on a target cell, by contacting the pharmaceutical
 CC composition in vitro, ex vivo or in vivo by administering the composition
 CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
 CC on the target cell. The agent or the composition is useful for treating a
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
 CC tumour cell. The invention is also useful for inhibiting an activity of
 CC NK cell or a T-cell. The present sequence is rat MAFA protein

XX SQ Sequence 188 AA;

Query Match 100.0%; Score 1036; DB 4; Length 188;
 Best Local Similarity 100.0%; Pred. No. 1.8e-96;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNSYSTLELPAAAPRVQDDSRWKVAVLHRRPCVSYLVNVALGLLTVILMSLLLYQRTL 60
 DB 1 MADNSYSTLELPAAAPRVQDDSRWKVAVLHRRPCVSYLVNVALGLLTVILMSLLLYQRTL 60

QY 61 CCGSKGFMCSQCRCPNLWNRNGSHCYFYSMEKRDWNSLKFCDKSGSHLLTFPDNOGVN 120
 DB 61 CCGSKGFMCSQCRCPNLWNRNGSHCYFYSMEKRDWNSLKFCDKSGSHLLTFPDNOGVN 120

QY 121 LFOEYVGEDFYWIGLRIDGWRWEDGPALSLSLNSVVKCGTIHRCGLHASSCEVALQ 180
 DB 121 LFOEYVGEDFYWIGLRIDGWRWEDGPALSLSLNSVVKCGTIHRCGLHASSCEVALQ 180

QY 181 WICEKVL 188
 DB 181 WICEKVL 188

RESULT 4
 AAE11760
 ID AAE11760 standard; protein; 188 AA.
 XX AC AAE11760;
 DT 18-DEC-2001 (first entry)
 XX DE Mouse mast cell function associated antigen (MAFA) protein.
 XX KW Mouse; pharmaceutical composition; mast cell function associated antigen;
 XX KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
 XX KW immunosuppressive; cytostatic.
 XX OS Mus sp.
 XX Key Location/Qualifiers
 FT Domain 64..188
 FT /note= "Extracellular domain"
 XX WO200170805-A2.
 XX 27-SEP-2001.
 XX 16-MAR-2001; 2001WO-US008596.
 XX 17-MAR-2000; 2000US-0190716P.
 XX (GEMI-) GEMINI SCI INC.
 XX Takahashi N, Mikayama T;
 XX WPI; 2001-611482/70.
 XX N-PSDB; AAD18735.
 XX Pharmaceutical composition for treating tumor by stimulating cytotoxic
 PT activity of natural killer cell or T-cell, comprises an agent that binds
 PT to mast cell function-associated antigen ligand on target cell.
 XX Example 1; Page 19; 49pp; English.
 XX The present invention relates to a pharmaceutical composition comprising
 CC an agent which specifically binds to a mast cell function associated
 CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
 CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
 CC ligand and a pharmaceutically acceptable excipient. The invention is
 CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
 CC binding to a ligand on a target cell, by contacting the pharmaceutical
 CC composition in vitro, ex vivo or in vivo by administering the composition

CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
 CC on the target cell. The agent or the composition is useful for treating a
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
 CC tumour cell. The invention is also useful for inhibiting an activity of
 CC NK cell or a T-cell. The present sequence is mouse MAFA protein

XX SQ Sequence 188 AA;

Query Match 80.9%; Score 838; DB 4; Length 188;
 Best Local Similarity 80.7%; Pred. No. 1.9e-76;
 Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADNSYSTLELPAAAPRVQDDSRWKVAVLHRRPCVSYLVNVALGLLTVILMSLLLYQRTL 60
 DB 1 MADNSYSTLELPAAAPRVQDDSRWKVAVLHRRPCVSYLVNVALGLLTVILMSLLLYQRTL 60

QY 61 CCGSKGFMCSQCRCPNLWNRNGSHCYFYSMEKRDWNSLKFCDKSGSHLLTFPDNOGVN 120
 DB 61 CCGSKGFMCSQCRCPNLWNRNGSHCYFYSMEKRDWNSLKFCDKSGSHLLTFPDNOGVN 120

QY 121 LFOEYVGEDFYWIGLRIDGWRWEDGPALSLSLNSVVKCGTIHRCGLHASSCEVALQ 180
 DB 121 LFOEYVGEDFYWIGLRIDGWRWEDGPALSLSLNSVVKCGTIHRCGLHASSCEVALQ 180

QY 181 WICEKVL 187
 DB 181 WICKVL 187

RESULT 5
 AAR77472
 ID AAR77472 standard; protein; 114 AA.
 XX AC AAR77472;
 DT 01-FEB-1996 (first entry)
 XX DE Partial sequence of mast cell function-associated antigen (MAFA).
 XX KW Mast cell function-associated antigen; MAFA; soluble; ligand;
 XX KW identification; screening; inflammation; inflammatory; allergy; allergic;
 XX KW prevention.
 XX OS Rattus rattus.
 XX WO9527734-A1.
 XX 19-OCT-1995.
 XX 06-APR-1995; 95WO-US004258.
 XX 08-APR-1994; 94IL-00109257.
 XX (YEDA) YEDA RES & DEV CO LTD.
 XX (RYCU/) RYCU S A.
 XX Pecht I, Guthmann MD, Tal M;
 XX WPI; 1995-366356/47.
 XX N-PSDB; AAT01471.
 XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -
 PT useful for screening for ligands of MAFA which are useful for prevention
 PT of inflammatory and allergic reactions.
 XX Disclosure; Page 38; 54pp; English.
 XX A soluble form of mast cell function-associated antigen (MAFA) can be
 CC produced by recombinant techniques for use in the ligand- screening
 CC assay. The ligands that are identified may be used alone or in
 CC combination with the MAFA to prevent inflammatory and allergic reactions

```

XX SQ Sequence 114 AA;
Query Match 62.8%; Score 651; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 8.1e-58;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 CPNLWRNGSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGVNLFQEVYGVDFYWG 134
DB 1 CPNLWRNGSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGVNLFQEVYGVDFYWG 60

QY 135 LRDIDGWRWEDGPAISLSILNSVVKQCTHRCGLHASSCEVALQWICEKVL 188
DB 61 LRDIDGWRWEDGPAISLSILNSVVKQCTHRCGLHASSCEVALQWICEKVL 114

RESULT 6
ADD25635
ID ADD25635 standard; protein; 189 AA.
XX AC
XX AC ADD25635;
XX DT
XX DT 15-JAN-2004 (first entry)
XX DE Binding domain-immunoglobulin fusion protein-associated protein #95.
XX KW Binding domain; immunoglobulin; fusion protein; cytostatic;
XX KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
XX KW neuroprotective; hinge region; immunoglobulin heavy chain;
XX KW CH2 constant region; CH3 constant region; IgG1;
XX KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
XX KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
XX KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
XX KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX OS Unidentified.
XX FN US2003118592-A1.
XX PD 26-JUN-2003.
XX PF 25-JUL-2002; 2002US-00207655.
XX PR 17-JAN-2001; 2001US-0367358P.
XX PR 17-JAN-2002; 2002US-00053530.
XX PR 03-JUN-2002; 2002US-0385691P.
XX PA (GENE-) GENE-CRAFT INC.
XX FI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX DR WPI; 2003-801317/75.
XX PT New binding domain-immunoglobulin fusion protein, useful for treating a
XX PT subject having or suspected of having a malignant condition or a B-cell
XX PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX PS Disclosure; SEQ ID NO 196; 157pp; English.
XX CC The invention relates to a binding domain-immunoglobulin fusion protein
XX CC comprising a binding domain polypeptide that is fused to an
XX CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
XX CC CH2 constant region polypeptide that is fused to the hinge region
XX CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
XX CC polypeptide that is fused to the CH2 constant region polypeptide. The
XX CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
XX CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
XX CC region polypeptide, derived from (a) having 3 or more cysteine residues;
XX CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
XX CC contains 2 cysteine residues, where the first cysteine is not mutated; a
XX CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
XX CC (a) having 3 or more cysteine residues, where the mutated human IgG1
XX CC immunoglobulin hinge region polypeptide contains no more than one
cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
polypeptide, derived from (a) having 3 or more cysteine residues; where
the mutated human IgG1 immunoglobulin hinge region polypeptide contains
no cysteine residues. The binding domain-immunoglobulin fusion protein is
capable of at least one immunological activity comprising antibody
dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
binding domain polypeptide is capable of specifically binding to an
antigen. Also included are an isolated polynucleotide encoding the
binding domain-immunoglobulin fusion protein, a recombinant expression
construct comprising the polynucleotide (operably linked to a promoter),
a host cell transformed or transfected with a recombinant expression
construct, producing the binding domain-immunoglobulin fusion protein, a
pharmaceutical composition comprising the binding domain-immunoglobulin
fusion protein or polynucleotide and a carrier, and treating a subject
having or suspected of having a malignant condition or a B-cell disorder.
The binding domain-immunoglobulin fusion protein is useful for treating a
subject having or suspected of having a malignant condition or a B-cell
disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
sclerosis or autoimmune disease. The present sequence is a binding domain
-immunoglobulin fusion protein-associated protein sequence. Note: The
sequence data for this patent formed part of the printed specification
and is also available in electronic format directly from USPTO at
seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
identified the sequences in the printed specification by their SEQ ID
number therefore none of the sequences can be explicitly identified.
XX SQ Sequence 189 AA;
Query Match 52.7%; Score 545.5; DB 7; Length 189;
Best Local Similarity 55.1%; Pred. No. 7.1e-47;
Matches 103; Conservative 28; Mismatches 55; Indels 1; Gaps 1;

QY 1 MADNSIYSLTLELPAPRVQDDSRWKVAVLHRCVSVLYVVALGLTLVILSLIYQRTL 60
DB 1 MTSVIYSMLELPTAQNDYGPQKSSSRSPSCSLVALGTLAVLSVLLYQWIL 60

QY 61 CCGSKGFMCQSCPCPNLWNRNGSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGVN 120
DB 61 CQSNYSTCASCPCSPDRWKVAVLHRCVSVLYVVALGLTLVILSLIYQRTL 120

QY 121 LFOYVGEDFYWIGLRDIDGWRWEDGPAISLSILNSVVKQCTHRCGLHASSCEVAL 179
DB 121 LQVFLSEAFQWICGLRNNSGWRWEDGPAISLSILNSVVKQCTHRCGLHASSCEVAL 180

QY 180 QWICEKV 186
DB 181 HWCKKV 187

RESULT 7
AAW88265
ID AAW88265 standard; protein; 189 AA.
XX AC
XX AC AAW88265;
XX DT
XX DT 29-MAR-1999 (first entry)
XX DE Human mast cell function-associated antigen (MAFA).
XX KW Mast cell function-associated antigen; MAFA; splice variant; human;
XX KW inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 7..10
XX FT Modified-site 65..67
XX FT Modified-site 97..99
XX FT Modified-site 137..139

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```
FT      /note= "Asn is N-glycosylated"
FT      150..152
FT      /note= "Asn is N-glycosylated"
XX
XX
XX      WO9854209-A2.
XX
XX      03-DEC-1998.
XX
XX      29-MAY-1998; 98WO-GB001572.
XX
XX      31-MAY-1997; 97GB-00011148.
XX
XX      (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX      Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
XX
XX      WPI; 1999-059806/05.
XX      N-PSDB; AAV84198.
XX
XX      New polypeptide having a sequence corresponding to human mast cell
XX      function-associated antigen - useful in forming and manufacturing
XX      pharmaceutical compositions in the treatment of inflammatory and allergic
XX      diseases, and tumour growth.
XX
XX      Disclosure; Fig 1; 44pp; English.
XX
XX      This is the amino acid sequence of human mast cell function- associated
XX      antigen (MAFA), a type II membrane glycoprotein. cDNA (see AAV84198)
XX      encoding human MAFA can be obtained from myelogenous leukaemic cell line
XX      KU812 or cDNA derived from human lung tissue. The encoded protein is
XX      similar to the rat form (see AAW88277) having an intracellular domain
XX      containing a putative immunoreceptor tyrosine activation motif (ITIM) and
XX      an extracellular lectin-like domain. 2 Alternatively spliced forms (see
XX      AAW88266-67) of human MAFA have been identified. Polypeptides and
XX      synthetic peptides (see AAW88258-64) based on these truncated MAFA
XX      proteins can be used in methods for the treatment of inflammatory and
XX      allergic diseases, and tumour growth
XX
XX      Sequence 189 AA;
XX
XX      Query Match      50.7%; Score 525.5; DB 2; Length 189;
XX      Best Local Similarity 53.5%; Pred. No. 7.4e-45;
XX      Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;
XX
XX      QY      1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRPCVSYLVNVALGLLTVILMSLLLYQRTL 60
XX      | : | | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
XX      Db      1 MTDSVIYSMLELPTATQAQNDYGPQKSSSKPSCSLVAITLGLLTAVLLSYLQWIL 60
XX      | : | | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
XX      QY      61 CCSGKGFMCSCQRCPNLWNRNGSHCYFFSMEKRDWNSLKFCADKGSLLTTPDNOGVN 120
XX      | : | | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
XX      Db      61 CQGSNYSTCASCPCPDPRWKYGNHCYFFSVEEKDWNSSLEFCLARDSHLLVITDNGMS 120
XX      | : | | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
XX      QY      121 LFOEYVGEDFYWIGRIDGMRWEDGPALSLS-ILNSVYVKCGTTHRCGLHASSCEVAL 179
XX      | : | | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
XX      Db      121 LLQVFLSEAFWIGLRNNSGMRWEDGSPNLSFSSNFSVQTGAINKNGQLQASSCEVPL 180
XX      | : | | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
XX      QY      180 QWICEKV 186
XX      : | : | |
XX      Db      181 HGVCCKV 187
XX      : | : | |
XX
XX      RESULT 8
XX      AAE11759
XX      ID AAE11759 standard; protein; 189 AA.
XX      AC AAE11759;
XX      AC
XX      DT 18-DEC-2001 (first entry)
XX      DE Human mast cell function associated antigen (MAFA) protein.
XX      KW Human; pharmaceutical composition; mast cell function associated antigen;
XX      KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
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XX      immunosuppressive; cytostatic.
XX      Homo sapiens.
XX      WO200170805-A2.
XX      27-SEP-2001.
XX
XX      16-MAR-2001; 2001WO-US008596.
XX
XX      17-MAR-2000; 2000US-0190716P.
XX      (GEMI-) GEMINI SCI INC.
XX
XX      Takahashi N, Mikayama T;
XX
XX      WPI; 2001-611482/70.
XX      N-PSDB; AAD18734.
XX
XX      Pharmaceutical composition for treating tumor by stimulating cytotoxic
XX      activity of natural killer cell or T-cell, comprises an agent that binds
XX      to mast cell function-associated antigen ligand on target cell.
XX
XX      Claim 10; Page 18; 49pp; English.
XX
XX      The present invention relates to a pharmaceutical composition comprising
XX      an agent which specifically binds to a mast cell function associated
XX      antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
XX      killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
XX      ligand and a pharmaceutically acceptable excipient. The invention is
XX      useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
XX      binding to a ligand on a target cell, by contacting the pharmaceutical
XX      composition in vitro, ex vivo or in vivo by administering the composition
XX      to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
XX      an amount sufficient to inhibit cell surface MAFA binding to the ligand
XX      on the target cell. The agent or the composition is useful for treating a
XX      tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
XX      T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
XX      tumour cell. The invention is also useful for inhibiting an activity of
XX      NK cell or a T-cell. The present sequence is human MAFA protein
XX
XX      Sequence 189 AA;
XX
XX      Query Match      50.7%; Score 525.5; DB 4; Length 189;
XX      Best Local Similarity 53.5%; Pred. No. 7.4e-45;
XX      Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;
XX
XX      QY      1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRPCVSYLVNVALGLLTVILMSLLLYQRTL 60
XX      | : | | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
XX      Db      1 MTDSVIYSMLELPTATQAQNDYGPQKSSSKPSCSLVAITLGLLTAVLLSYLQWIL 60
XX      | : | | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
XX      QY      61 CCSGKGFMCSCQRCPNLWNRNGSHCYFFSMEKRDWNSLKFCADKGSLLTTPDNOGVN 120
XX      | : | | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
XX      Db      61 CQGSNYSTCASCPCPDPRWKYGNHCYFFSVEEKDWNSSLEFCLARDSHLLVITDNGMS 120
XX      | : | | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
XX      QY      121 LFOEYVGEDFYWIGRIDGMRWEDGPALSLS-ILNSVYVKCGTTHRCGLHASSCEVAL 179
XX      | : | | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
XX      Db      121 LLQVFLSEAFWIGLRNNSGMRWEDGSPNLSFSSNFSVQTGAINKNGQLQASSCEVPL 180
XX      | : | | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
XX      QY      180 QWICEKV 186
XX      : | : | |
XX      Db      181 HGVCCKV 187
XX      : | : | |
XX
XX      RESULT 9
XX      ABG05451
XX      ID ABG05451 standard; protein; 843 AA.
XX      AC ABG05451;
XX      AC
XX      DT 13-FEB-2002 (first entry)
XX      DE Novel human diagnostic protein #5442.
```


CC The invention relates to a novel isolated polypeptide, designated NOVX
 CC (NOV1 - 33), consisting of a mature form of one of si sequences, given in
 CC the specification, or its variant, where amino acid residue(s) in the
 CC variant differ from the mature form, provided that the variant differs in
 CC not more than 15 % of the amino acids from the sequence of the mature
 CC form. The NOVX polypeptides, nucleic acids encoding the polypeptides, and
 CC an antibody to the polypeptides, are useful for treating or preventing a
 CC NOVX-associated disorder in humans and for treating a syndrome associated
 CC with a human disease (NOVX-associated disorder). NOVX polypeptides and
 CC the encoding nucleic acids, are useful for determining the presence of or
 CC predisposition to a disease associated with altered levels of NOVX
 CC polypeptide and polynucleotide, by measuring the level of polypeptide
 CC expression or the amount of nucleic acid from a mammal and comparing it
 CC with another mammal not having or not predisposed to the disease. NOVX
 CC polypeptide is also useful for identifying an agent that binds to NOVX
 CC and a cell expressing NOVX is useful for identifying an agent that
 CC modulates the expression or activity of NOVX. The antibodies and a
 CC polypeptide having 95 % sequence identity to NOVX polypeptide are useful
 CC for treating a pathological state in a mammal. The antibodies are also
 CC useful for determining the presence or amount of NOVX in a sample. NOVX
 CC polypeptides, polynucleotides and antibodies specific for the
 CC polypeptides are useful for treating or preventing disorders or syndromes
 CC including trauma, viral, bacterial, fungal, protozoal, and parasitic
 CC infections. They can also treat disorders such as e.g., Alzheimer's
 CC disease or a stroke. The NOVX encoding nucleic acids are useful for
 CC expressing the NOVX proteins, to detect NOVX mRNA, or a genetic lesion in
 CC a NOVX gene and to modulate NOVX activity. NOVX sequences are also useful
 CC for identifying a cell or tissue type in a biological sample, to amplify
 CC DNA sequences from very small biological samples such as tissues e.g.
 CC hair or skin or body fluids in forensic biology and as primers and probes
 CC for use in identifying and/or cloning NOVX homologues in other cell
 CC types. The NOVX proteins are useful as an immunogen to generate
 CC antibodies which are useful for diagnostically monitoring protein levels
 CC and modulating NOVX activity. Cells comprising NOVX nucleic acids are
 CC useful for producing non-human transgenic animals which are useful for
 CC studying the function and/or activity of NOVX protein and for identifying
 CC and/or evaluating modulators of NOVX protein activity. The NOVX nucleic
 CC acids can be used in gene therapy. This sequence represents a NOVX
 CC protein of the invention

XX SQ Sequence 191 AA;

Query Match 24.3%; Score 251.5; DB 6; Length 191;
 Best Local Similarity 31.4%; Pred. No. 3.8e-17;
 Matches 59; Conservative 24; Mismatches 84; Indels 21; Gaps 5;
 QY 12 LPAPRVQDDSRWKVAVL--HRPCVSY-LVMVALGLLTVILMSLLLYQRTLCGSGKGF 68
 Db 12 LPESQFESHORLVLLPILHVNKSYRMYSFCLGLFTLVROSLSLSPLECSGALSAH 71
 QY 69 CSQCSKCPNLWMRNGSHCYFYSMEKRDWNSLSLKFCADKGSLLTTFPDNQGVNLFQYVGE 128
 Db 72 CKICEPCPTSWLPFGSGCYFYSFKTTWBAQOHCADASAHAAFPEDRKVAFYSVLLGR 131
 QY 129 DFYWIGLRIDIGWRW-----DGPAL--SLSILSNVVKCGTTHRCGLHASSCEVAL 179
 Db 132 CLFGIGLARVGGWRVAPGTQIDAFVGGACFCQESI-----SGLPASELRLEK 182
 QY 180 QWICEKVL 187
 Db 183 WWHCSKTL 190

RESULT 11

AAW8267
 ID AAW8267 standard; protein; 99 AA.

AC AAW8267;

XX 29-MAR-1999 (first entry)

DT Human MAPA splice variant huMAFA(E3/4-).

KW Mast cell function-associated antigen; MAPA; huMAFA(E3/4-);
 KW splice variant; human; inflammation; allergy; asthma;
 KW rheumatoid arthritis; tumour; therapy.

OS Homo sapiens.

PN WO9854209-A2.

XX 03-DEC-1998.

PD 29-MAY-1998; 98WO-GB001572.

PF 31-MAY-1997; 97GB-00011148.

PR (PEPT-) PEPTIDE THERAPEUTICS LTD.

PA Hewitt EL, Lamers MBAC, Lamont A, Williams DH;

PI WPI; 1999-059806/05.

XX N-PSDB; AAV84200.

XX New polypeptide having a sequence corresponding to human mast cell
 PT function-associated antigen - useful in forming and manufacturing
 PT pharmaceutical compositions in the treatment of inflammatory and allergic
 PT diseases, and tumour growth.

XX Disclosure; Fig 3; 44pp; English.

XX This is the amino acid sequence of human mast cell function- associated
 CC antigen (MAPA) splice variant huMAFA(E3/4-), which lacks the C-lectin-
 CC like domain of human MAPA (see AAW8265) but retains the intracellular
 CC and transmembrane domains as well as the extracellular C-terminal tail.
 CC Truncated MAPA polypeptides including huMAFA(E3/4-), and polynucleotides
 CC encoding them, as well as synthetic peptides (see AAW8258-64, AAW8268-
 CC 72), can be used in compositions for the treatment of
 CC inflammatory and allergic diseases (e.g. rheumatoid arthritis and
 CC asthma), or tumour growth

XX Sequence 99 AA;

Query Match 20.0%; Score 207.5; DB 2; Length 99;
 Best Local Similarity 29.6%; Pred. No. 4.7e-13;
 Matches 55; Conservative 12; Mismatches 30; Indels 89; Gaps 1;
 QY 1 MADNSTYSTLELPAPRVQDDSRWKVAVLHRCVSYLVMVALGLLTVILMSLLLYQRTL 60
 Db 1 MTDSVIYSMLLELPATQAQNDYGPQKSSSRPSCSLVAIALGLLTAVLLSVLLYQWIL 60
 QY 61 CCGSKGFCMCSQCRCNLMWRNGSHCYFYSMEKRDWNSLSLKFCADKGSLLTTFPDNQGVN 120
 Db 61 CQG-----
 QY 121 LFOEYVGEDFYWIGLRIDIGWRWEDGPFALSLSILSNVVKCGTTHRCGLHASSCEVALQ 180
 Db 64 -----ISSNSFVQTCGATKNGLGQASSCEVPLH 91
 QY 181 WICEKV 186
 Db 92 WVCCKV 97

RESULT 12

AAW54659
 ID AAW54659 standard; protein; 199 AA.

XX AAW54659;

XX 25-MAR-2003 (revised)

DT 31-OCT-1994 (first entry)

XX Human CD69.

DE Immune system; thrombocyte development; signal transduction; probe;
 KW

KW assay; diagnosis; therapy.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Protein 79..199
 FT /note= "soluble polypeptide"
 XX
 XX WO9410188-A1.
 PN
 XX
 PD 11-MAY-1994.
 XX
 XX 28-OCT-1993; 93WO-US010418.
 PF
 XX 29-OCT-1992; 92US-00971097.
 PR
 XX (IMMV) IMMUNEX CORP.
 PA
 XX Ziegler SR, Hjerrild KA;
 PI
 XX WPI; 1994-167377/20.
 DR N-PSDB; AAQ65340.
 XX
 XX CD69 nucleic acids and polypeptide - used in the diagnosis, therapy and
 FT study of the activation and regulation of the immune system.
 PT
 XX
 XX Claim 10; Page 27; 35pp; English.
 PS
 XX The sequence is that of human CD69. The CD69 protein is active in the
 CC regulation and function of the immune system. The protein may be used for
 CC blocking thymocyte development in in vitro systems. The soluble
 CC polypeptide can be used to competitively bind the ligand in vivo thus
 CC inhibiting signal transduction activity via endogenous cell surface bound
 CC CD69. CD69 may also be used to generate antibodies. See also AAR54660.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 199 AA;

Query Match 17.8%; Score 184.5; DB 2; Length 199;
 Best Local Similarity 26.3%; Pred. No. 2.4e-10;
 Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;
 QY 35 VSYLVVALGLLTIVILMSLLLYQRTLCGSGGFC---SQSRCPNLMWRNGSHCYFPM 91
 Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
 45 VMNVVFTILLIALISVGQYN---CPGQYTFSPSDSHVSSCSDEDWVGQKCYFIST 101
 QY 92 EKRDNWSLKFCDKAGSHLLTFPDNQGNLFQEVYGEDFYWIGLRDIDG--WRWEDGPA 149
 Db || | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
 102 VKRSWTSQAQACSEHGATLAVIDSEKDMNFKRYAGREHVVGLKKEPQKNGKEF 161
 QY 150 SLSTLSNSVVKCGTIHRCGLHASSCEVALOWICEK 185
 Db : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
 162 N-NWFNVGTGDKCVFLKNTVEVSMCEKNLYWICNK 196

RESULT 13
 AAW85593
 ID AAW85593 standard; protein; 199 AA.
 XX
 AC AAW85593;
 XX
 XX 02-MAR-1999 (first entry)
 DT
 XX Human CD69.
 DE
 XX lectin; carbohydrate; binding; agglutination; selectin; receptor;
 KW calcium dependent binding; treatment; cancer; detection; identification;
 KW CTL-1; ovary; paraganglionic; penis; brain; thyroid; heart.
 XX
 XX Homo sapiens.
 OS
 XX WO9849306-A1.
 FN
 XX

PD 05-NOV-1998.
 XX
 XX 29-APR-1998; 98WO-US008791.
 XX
 XX 29-APR-1997; 97US-00846523.
 XX
 XX (INCY-) INCYTE PHARM INC.
 PA
 XX Bandman O, Shah P;
 PI
 XX WPI; 1999-024060/02.
 XX
 XX N-PSDB; AAV83109.
 DR
 XX New human C-type lectin and related nucleic acid, vectors, transformed
 PT cells - antibodies, agonists and antagonists, for diagnosis, prevention
 PT and treatment of cancers.
 XX
 XX Example 3; Page 48; 64pp; English.
 PS
 XX Human CD69 shows homology with the human CTL-1 protein sequence.
 CC Recombinant cells containing expression vectors comprising the CTL-1
 CC coding sequence can be used to produce recombinant CTL-1 which is useful
 CC for raising Ab and to screen for specific binding agents. Binding agents
 CC which are antagonists of CTL-1 can be used to treat or prevent cancer,
 CC e.g. of ovary, paraganglion, penis, brain, thyroid and heart which are
 CC associated with overexpression of CTL-1. Fragments of this sequence are
 CC used to diagnose these conditions, as probes or primers in usual
 CC hybridisation and/or amplification assays, or for gene mapping, while
 CC complements of this sequence, antisense or ribozyme sequences are used to
 CC treat or prevent the aforementioned cancers also. Ab are used directly as
 CC antagonists or for delivery of therapeutic agents to cells that express
 CC CTL-1. CTL-1 includes a carbohydrate-recognition domain (aa35-149) and
 CC also a transmembrane domain, but no secretory signal. CTL-1 also shows
 CC homology with chicken 17.5.3 (AAW85594), and mouse CD69 (AAW85595)
 CC proteins
 XX
 SQ Sequence 199 AA;

Query Match 17.8%; Score 184.5; DB 2; Length 199;
 Best Local Similarity 26.3%; Pred. No. 2.4e-10;
 Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;
 QY 35 VSYLVVALGLLTIVILMSLLLYQRTLCGSGGFC---SQSRCPNLMWRNGSHCYFPM 91
 Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
 45 VMNVVFTILLIALISVGQYN---CPGQYTFSPSDSHVSSCSDEDWVGQKCYFIST 101
 QY 92 EKRDNWSLKFCDKAGSHLLTFPDNQGNLFQEVYGEDFYWIGLRDIDG--WRWEDGPA 149
 Db || | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
 102 VKRSWTSQAQACSEHGATLAVIDSEKDMNFKRYAGREHVVGLKKEPQKNGKEF 161
 QY 150 SLSTLSNSVVKCGTIHRCGLHASSCEVALOWICEK 185
 Db : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
 162 N-NWFNVGTGDKCVFLKNTVEVSMCEKNLYWICNK 196

RESULT 14
 ADD25621
 ID ADD25621 standard; protein; 199 AA.
 XX
 AC ADD25621;
 XX
 XX 15-JAN-2004 (first entry)
 DT
 XX Binding domain-immunoglobulin fusion protein-associated protein #88.
 DE
 XX Binding domain; immunoglobulin; fusion protein; cytostatic;
 KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
 KW neuroprotective; hinge region; immunoglobulin heavy chain;
 KW CH2 constant region; CH3 constant region; IgG1;
 KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
 KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
 KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
 KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.

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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:18:53 ; Search time 40.2619 Seconds
(without alignments)
1464.718 Million cell updates/sec

Title: US-09-811-367B-5
Perfect score: 1036
Sequence: 1 MADNSYSTLELPAAPRVQD.....GLHASSCEVALQWICKVLP 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	9	US-09-811-367B-5
2	838	80.9	188	9	US-09-811-367B-3
3	545.5	52.7	189	14	US-10-207-655-196
4	525.5	50.7	189	9	US-09-811-367B-1
5	184.5	17.8	199	10	US-09-284-320-86
6	184.5	17.8	199	14	US-10-207-655-182
7	184.5	17.8	199	14	US-10-179-528-3
8	184.5	17.8	199	15	US-10-379-127-26
9	184	17.8	257	14	US-10-179-528-4
10	182	17.6	268	15	US-10-161-493-22
11	180	17.4	231	16	US-10-451-843-1
12	179.5	17.3	265	9	US-09-764-870-307
13	179.5	17.3	265	4	US-10-125-540-307
14	179.5	17.3	275	15	US-10-161-493-20
15	177.5	17.1	229	9	US-09-989-722-424

16	177.5	17.1	229	9	US-09-989-723-424	Sequence 424, App
17	177.5	17.1	229	9	US-09-989-279-424	Sequence 424, App
18	177.5	17.1	229	9	US-09-989-727-424	Sequence 424, App
19	177.5	17.1	229	9	US-09-989-731-424	Sequence 424, App
20	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
21	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
22	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
23	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
24	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
25	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
26	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
27	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
28	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
29	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
30	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
31	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
32	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
33	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
34	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
35	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App
36	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App
37	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App
38	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App
39	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App
40	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App
41	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App
42	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App
43	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App
44	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App
45	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App

ALIGNMENTS

RESULT 1

US-09-811-367B-5
; Sequence 5, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THE
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811.367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR FILING DATE: 2000-03-17
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-811-367B-5

Query Match	100.0%	Score 1036;	DB 9;	Length 188;
Best Local Similarity	100.0%	Pred. No. 2.7e-99;		
Matches 188;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MADNSYSTLELPAAPRVQDSEWVKAVLHRCPCVSYLVNVALGLLTVILMSLLYQRTL	60	
Db	1	MADNSYSTLELPAAPRVQDSEWVKAVLHRCPCVSYLVNVALGLLTVILMSLLYQRTL	60	
QY	61	CCGSKGFMCSQSRCPNLWRNGSHCHYFSMEKRDWNSLKFCADKXGSHLLTPPDNOGVN	120	
Db	61	CCGSKGFMCSQSRCPNLWRNGSHCHYFSMEKRDWNSLKFCADKXGSHLLTPPDNOGVN	120	
QY	121	LFQEVYGEDFYWITGLRDIDGWRWEDGPALSLSTLSNSVVKCGTTHRCGHHASSCEVALQ	180	
Db	121	LFQEVYGEDFYWITGLRDIDGWRWEDGPALSLSTLSNSVVKCGTTHRCGHHASSCEVALQ	180	

QY 181 WICEKVL 188
Db 181 WICEKVL 188

RESULT 2
US-09-811-367B-3
; Sequence 3, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-811-367B-3

Query Match 80.9%; Score 838; DB 9; Length 188;
Best Local Similarity 80.7%; Pred. No. 9.7e-79;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHPCVSYLVVVALGLLTVILMSLLLYQRTL 60
Db 1 MADSSIYSTLELPEAPQVQDESRRWKLKAVLHRLPHLSRFAMVALGLLTVILMSLLMYQRL 60

QY 61 CGSGKGFMCSCQSRCPNLWMRNGSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGVN 120
Db 61 CGSKDSTGSHPCPILWTRNGSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGVN 120

QY 121 LFOEYVGEDFYWIGLRDIDGWRWEDGPALSLSILNSVVKCGTHRCGLHASSCEVALQ 180
Db 121 LFGELYGQDFYWIGLRNIDGWEGGPALSLSILNSLQRCGAIHRNGLOASSCEVALQ 180

QY 181 WICEKVL 187
Db 181 WICEKVL 187

RESULT 3
US-10-207-655-196
; Sequence 196, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 196
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-196

Query Match 52.7%; Score 545.5; DB 14; Length 189;
Best Local Similarity 55.1%; Pred. No. 2.3e-48;
Matches 103; Conservative 28; Mismatches 55; Indels 1; Gaps 1;

QY 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHPCVSYLVVVALGLLTVILMSLLLYQRTL 60
Db 1 MTDSVIYSMLLELPTAQNDYGPQKSSSSRSCCLVATLGLTAVLLSVLLYQWIL 60

QY 61 CGSGKGFMCSCQSRCPNLWMRNGSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGVN 120
Db 61 CQGSNYSTCASCPCPDPRWKYGNHCYFYSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120

QY 121 LFOEYVGEDFYWIGLRDIDGWRWEDGPALSLSILNSVVKCGTHRCGLHASSCEVAL 179
Db 121 LLQVFLSEAFWCWIGLRNNSGWRWEDGSPNFSRISNSFVQTCGAINKNGLOASSCEVPL 180

QY 180 QWICEKV 186
Db 181 HWCKKV 187

RESULT 4
US-09-811-367B-1
; Sequence 1, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-367B-1

Query Match 50.7%; Score 525.5; DB 9; Length 189;
Best Local Similarity 53.5%; Pred. No. 2.7e-46;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHPCVSYLVVVALGLLTVILMSLLLYQRTL 60
Db 1 MTDSVIYSMLLELPTAQNDYGPQKSSSSRSCCLVATLGLTAVLLSVLLYQWIL 60

QY 61 CGSGKGFMCSCQSRCPNLWMRNGSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGVN 120
Db 61 CQGSNYSTCASCPCPDPRWKYGNHCYFYSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120

QY 121 LFOEYVGEDFYWIGLRDIDGWRWEDGPALSLSILNSVVKCGTHRCGLHASSCEVAL 179
Db 121 LLQVFLSEAFWCWIGLRNNSGWRWEDGSPNFSRISNSFVQTCGAINKNGLOASSCEVPL 180

QY 180 QWICEKV 186
Db 181 HWCKKV 187

RESULT 5
US-09-284-320-86
; Sequence 86, Application US/09284320
; Publication No. US20030092175A1
; GENERAL INFORMATION:
; APPLICANT: Kato, Seishi et al.
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs
; FILE REFERENCE: GIN-6705CPUS
; CURRENT APPLICATION NUMBER: US/09/284,320
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: JP 8-301429

```
; PRIOR FILING DATE: 1996-11-13
; PRIOR APPLICATION NUMBER: PCT/JP97/04056
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 86
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-284-320-86

Query Match      17.8%; Score 184.5; DB 10; Length 199;
Best Local Similarity 26.3%; Pred. No. 7.2e-11;
Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;

QY 35 VSYLVWVALGLLTVILMSLLLYQRTLCGSGKGMFC---SQCRCFNIWMRNGSHCYFFSM 91
   | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 45 VMNVVFITILIALISVGQYN---CPGQYTFSPSDSHVSSCSDEDWVGQYQKCYFIST 101
   | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 92 EKRDWNSSLKFCADKGSLLTFFPDNQGVNLFQEVVGDFYWGIGLRDIDG--WRWEDGPAL 149
   | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 102 VKRSWTSQAQACSEHGATLAVIDSEKDMNFKRYAGREHVGVLKPEGHPKWSNGKEF 161
   | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 150 SLSILSNVVKCGTTHRCGLHASSCEVALQWICEK 185
   | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 162 N-NWFNVGTGDKCVFLKNTVSSMECEKNLYWICNK 196
   | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 6
US-10-207-655-182
; Sequence 182, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 182
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-182

Query Match      17.8%; Score 184.5; DB 14; Length 199;
Best Local Similarity 26.3%; Pred. No. 7.2e-11;
Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;

QY 35 VSYLVWVALGLLTVILMSLLLYQRTLCGSGKGMFC---SQCRCFNIWMRNGSHCYFFSM 91
   | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 45 VMNVVFITILIALISVGQYN---CPGQYTFSPSDSHVSSCSDEDWVGQYQKCYFIST 101
   | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 92 EKRDWNSSLKFCADKGSLLTFFPDNQGVNLFQEVVGDFYWGIGLRDIDG--WRWEDGPAL 149
   | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 102 VKRSWTSQAQACSEHGATLAVIDSEKDMNFKRYAGREHVGVLKPEGHPKWSNGKEF 161
   | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 150 SLSILSNVVKCGTTHRCGLHASSCEVALQWICEK 185
   | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 162 N-NWFNVGTGDKCVFLKNTVSSMECEKNLYWICNK 196
   | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 7
US-10-179-528-3
; Sequence 3, Application US/10179528
; Publication No. US20030166136A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 7
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/179,528
; FILING DATE: 24-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,523
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0281 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 291898
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-179-528-3

Query Match      17.8%; Score 184.5; DB 14; Length 199;
Best Local Similarity 26.3%; Pred. No. 7.2e-11;
Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;

QY 35 VSYLVWVALGLLTVILMSLLLYQRTLCGSGKGMFC---SQCRCFNIWMRNGSHCYFFSM 91
   | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 45 VMNVVFITILIALISVGQYN---CPGQYTFSPSDSHVSSCSDEDWVGQYQKCYFIST 101
   | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 92 EKRDWNSSLKFCADKGSLLTFFPDNQGVNLFQEVVGDFYWGIGLRDIDG--WRWEDGPAL 149
   | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 102 VKRSWTSQAQACSEHGATLAVIDSEKDMNFKRYAGREHVGVLKPEGHPKWSNGKEF 161
   | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 150 SLSILSNVVKCGTTHRCGLHASSCEVALQWICEK 185
   | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 162 N-NWFNVGTGDKCVFLKNTVSSMECEKNLYWICNK 196
   | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 8
US-10-379-127-26
; Sequence 26, Application US/10379127
; Publication No. US20040005592A1
; GENERAL INFORMATION:
; APPLICANT: Emtage, Peter C.R.
; APPLICANT: Drmanac, Radoje
; APPLICANT: Goodrich, Ryle
; APPLICANT: Tang, Y. Ton
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THERAPY AND DIAGNOSIS USING TAR
; FILE REFERENCE: NUVO-01CIP
; CURRENT APPLICATION NUMBER: US/10/379,127
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 27
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-127-26

Query Match 17.8%; Score 184.5; DB 15; Length 199;
Best Local Similarity 26.3%; Pred. No. 7.2e-11;
Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;
QY 35 VSYLVNVALGGLTIVILMSLLLYQRTLCGSKGFMCGMC---SQSRCPENLWRRNGSHCHYFSM 91
DB 45 VMNVVFITILLIALIALSVGQYN---CPGQYTFSPSDSHVSSCSDEDWVGCRKCYFIST 101
QY 92 EKRDWNSLKFCADKSGHLLTFPDNQGNVLFQYVGEDFYWIGLRDIDG---WRWEDGSPAL 149
DB 102 VKRWSQAQACSEHGATLVIDSEKDMNFKRYAGREHWVGLKKEGHPKWSNGKEF 161
QY 150 SLSILSNSVQKCGTHRCGLHASSCEVALQWICEK 185
DB 162 N-NWNTVTSKCVFKRTEVSSMECKNLWICNK 196

RESULT 9

US-10-179-528-4
; Sequence 4, Application US/10179528
; Publication No. US20030166136A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Shah, Purvi
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/179,528
; FILING DATE: 24-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,523
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0281 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 505325
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-179-528-4

Query Match 17.8%; Score 184; DB 14; Length 257;

Best Local Similarity 28.6%; Pred. No. 1.1e-10;
Matches 46; Conservative 23; Mismatches 66; Indels 26; Gaps 6;
QY 33 PCVSYLVNVALGGLTIVILMSLLLYQRTLCGSKGFMCGSQSRCPENLWRRNGSHCHYFSME 92
DB 101 PC-----MLVLALVAVIVL-----QRPSCSPRPFP-----SHVCNNAVWVGFOCKCYFSDT 146
QY 93 KRDWNSLKFCADKSGHLLTFPDNQGNVLFQYVGEDFYWIGLRDIDG---WRWEDGSPAL 149
DB 147 ESDWNSREHCHRLGASLATLDTKEEMEFMLQYQRPADRWLGLHRAEGDEHWTWADGSF 206
QY 150 SLSILSNSVQKCGTHRCGLHASSCEVALQWICEK 185
DB 207 T-----NRVPFELRGGRCAVLNGDGISSALCHSEKFWVCSR 243

RESULT 10

US-10-161-493-22
; Sequence 22, Application US/10161493
; Publication No. US20040018555A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Zernhusen, Bryan D
; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
; APPLICANT: Casman, Stacie J
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shinkets, Richard A
; APPLICANT: Gorman, Linda
; APPLICANT: Pena, Carol EA
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leite, Mario W
; APPLICANT: Kastelli, Luca
; APPLICANT: MacDougall, John R
; APPLICANT: Taupier Jr., Raymond J
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Miller, Charles E
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Hjalt, Tord
; APPLICANT: Voss, Edward Z
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Ji, Weizhen
; APPLICANT: Smithson, Glennda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; TITLE OF INVENTION: No. US20040018555A1el Antibodies that Bind to Antigenic Polypept
; TITLE OF INVENTION: Acids Encoding the Antigens, and Methods of Use
; FILE REFERENCE: 21402-377A
; CURRENT APPLICATION NUMBER: US/10/161,493
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/337,524
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,575
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/359,151
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/297,414
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/297,573
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/341,143
; PRIOR FILING DATE: 2001-12-14


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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 299
; SEQ ID NO 20
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-493-20

Query Match      17.3%   Score 179.5; DB 15; Length 275;
Best Local Similarity 31.5%; Pred No. 3.5e-10;
Matches 41; Conservative 22; Mismatches 56; Indels 11; Gaps 5;

Qy      67 FMCQSCRCPLNMRNGSHCYFYSM-EKRDWNSSLKTCADKSGHLLTFP--DNQGVNLFQ 123
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; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
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; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Zernhusen, Bryan D
; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
; APPLICANT: Casman, Stacie J
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shimkets, Richard A
; APPLICANT: Gorman, Linda
; APPLICANT: Pena, Carol EA
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leite, Mario W
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R
; APPLICANT: Taupier Jr., Raymond J
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Miller, Charles E
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Hjalt, Tord
; APPLICANT: Voss, Edward Z
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Ji, Weizhen
; APPLICANT: Smithson, Glennda
; APPLICANT: Edinger, Salomit R
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; TITLE OF INVENTION: No. US20040018555A1el Antibodies that Bind to Antigenic Polypepti
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; CURRENT APPLICATION NUMBER: US/10/161,493
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GenCore version 5.1.6
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

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Listing first 45 summaries

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SUMMARIES

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45 148 14.3 237 3 US-09-111-470-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-722-126A-5
; Sequence 5, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-722-126A-5
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5  ; APPLICANT:
6  ; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
7  ; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
8  ; NUMBER OF SEQUENCES: 10
9  ; CORRESPONDENCE ADDRESS:
10 ; ADDRESSEE: BROWDY AND NEIMARK
11 ; STREET: 419 Seventh Street, N.W., Suite 300
12 ; CITY: Washington
13 ; STATE: D.C.
14 ; COUNTRY: USA
15 ; ZIP: 20004
16 ; COMPUTER READABLE FORM:
17 ; MEDIUM TYPE: Floppy disk
18 ; COMPUTER: IBM PC compatible
19 ; OPERATING SYSTEM: PC-DOS/MS-DOS
20 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
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23 ; FILING DATE: 06-APR-1995
24 ; PRIOR APPLICATION DATA:
25 ; APPLICATION NUMBER: IL 109257
26 ; FILING DATE: 08-APR-1994
27 ; ATTORNEY/AGENT INFORMATION:
28 ; NAME: BROWDY, Roger L.
29 ; REGISTRATION NUMBER: 25,618
30 ; REFERENCE/POCKET NUMBER: PECHT=1 PCT
31 ; TELECOMMUNICATION INFORMATION:
32 ; TELEPHONE: 202-628-5197
33 ; TELEFAX: 202-737-3528
34 ; TELEX: 248633
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37 ; LENGTH: 188 amino acids
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39 ; TOPOLOGY: linear
40 ; MOLECULE TYPE: protein
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; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996

```

RESULT 4
PCT-US95-04258-6

; Sequence 6, Application PC/TUS9504258
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PCHT=1 PCT
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-04258-6
; Query Match 62.8%; Score 651; DB 5; Length 114;
; Best Local Similarity 100.0%; Pred. No. 9.7e-64;
; Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 75 CPNLMWRNGSHCYFYSMEKRDWNSLKFCDKSGHLLTFPDNQGNLFOEYVGDYFYG 134
Db 1 CPNLMWRNGSHCYFYSMEKRDWNSLKFCDKSGHLLTFPDNQGNLFOEYVGDYFYG 60
Qy 135 LRIDGWRWEDGPAISLSILNSVVKCGTTHRCGLHASSCEVALQWICEKVL 198
Db 61 LRIDGWRWEDGPAISLSILNSVVKCGTTHRCGLHASSCEVALQWICEKVL 114
RESULT 5
US-09-531-056A-23
; Sequence 23, Application US/09531056A
; Patent No. 6455883
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531.056A
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 23
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-531-056A-23

Query Match 26.4%; Score 273; DB 4; Length 76;
Best Local Similarity 59.7%; Pred. No. 1.4e-22;
Matches 43; Conservative 14; Mismatches 15; Indels 0; Gaps 0;
Qy 75 CPNLMWRNGSHCYFYSMEKRDWNSLKFCDKSGHLLTFPDNQGNLFOEYVGDYFYG 134
Db 3 CPDWMKYGNHCYFYSVEEKDWSLSLEFCLARDSHLLVITDQMSLLQVFLSEAFCWIG 62
Qy 135 LRIDGWRWEDG 146
Db 63 LRNMSGWRWEDG 74
RESULT 6
PCT-US93-10418-2
; Sequence 2, Application PC/TUS9310418
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Steven F.
; APPLICANT: Hjerild, Kathryn A.
; TITLE OF INVENTION: Activation Antigen CD69
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10418
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2610-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-10418-2
; Query Match 17.8%; Score 184.5; DB 5; Length 199;
Best Local Similarity 26.3%; Pred. No. 2.4e-12;
Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;
Qy 35 VSVLVMVALGLLTVILMSLLYQRTLCCKSGKGFMC---SQCSRCPNLMWRNGSHCYFYSM 91
Db 45 VMNVVFTILLIALLSVQYN---CPGQVTFMPSDSHVSSCEDSHVGVQKCYFIST 101
Qy 92 EKRDWNSLKFCDKSGHLLTFPDNQGNLFOEYVGDYFYGIRLDIG--WRWEDGPA 149
Db 102 VKRSWTSQAQACSEHGATLAVIDSEKDMNFKRYAGREHVVGLKKEPGHPKWSNGKEF 161
Qy 150 SLSLNSVVKCGTTHRCGLHASSCEVALQWICEK 185
Db 162 N-NWFNTVGSCKVFLKNTVSSWECEKNLYWICNK 196
RESULT 7
US-08-772-440-13
; Sequence 13, Application US/08772440
; Patent No. 6046158

GENERAL INFORMATION:
APPLICANT: Ariizumi, Kiyoshi
APPLICANT: Takashima, Akira
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,440
FILING DATE: CONCURRENTLY HERewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTXD:493
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-772-440-13

Query Match 16.9%; Score 175.5; DB 3; Length 199;
Best Local Similarity 26.2%; Pred. No. 2.3e-11;
Matches 53; Conservative 32; Mismatches 74; Indels 43; Gaps 11;
QY 7 YSTLEPAAPRVQD-----DSRWKVKAVLHRCPCVSYLVMAVGLL--TVILMSLLLYOR 58
DB 20 FSTQDIHKPRSEKSRAPSPW-----RP-----IAGLGILCFVWVVAVL--- 64
QY 59 TLCCGSKGPMQCSCRCPLNWRNGSHCYFYSMEKRDWNSLKFCADKGSLLTTPDNQG 118
DB 65 ----GALGFGSQSC--LPN-WIMHGKSCYLFSGNSWYSGKXKHCSQLGAHLLKIDNSKE 117
QY 119 VNLFOEYVGE---DFWYIGU--RDIDG-WRWEDGPA-----LSLSILSNSVVKCGTI 165
DB 118 FEFIESQTSRRINAFWIGLSNQSGPWFWDGSAFFPNSFQVRNTVPQESLLHNCVWI 177
QY 166 HRCGLHASSCEVALOWICEKVL 187
DB 178 HGEVYNQICNTSSYSICEKEL 199

RESULT 8
US-09-247-155-97
Sequence 97, Application US/09247155A
Patent No. 6312922
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET 021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09

EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 97
LENGTH: 229
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: 47...1
US-09-247-155-97

Query Match 16.9%; Score 175.5; DB 4; Length 229;
Best Local Similarity 26.9%; Pred. No. 2.8e-11;
Matches 61; Conservative 32; Mismatches 83; Indels 51; Gaps 12;
QY 1 MADNSIYSTLEL---PAAPRVQDDSR--WKVKA-VLHRCPCVSYLV-MVALGLLTVILMS 52
DB 1 MDEDEGYITLNIKTRKPAIVSVGPASFWWRVMAILILLCVMVVGLVALGIWVMQRN 60
QY 53 LLLYQRTLCCGS-----KG-FMCSQCSCRCPLNWRNGSHCYFYSMEK 93
DB 61 YLDENENRTGLQOLAKRFQCYVYVQSELKGTFFKGHKSCPDITWRYYGDSYGFRRHN 120
QY 94 RDWNSSLKFCADKGSLLTTPDNQGVNLFQEVVGBDFY---WIGL---RDIDGWRWEDGP 147
DB 121 LTWEESKQYCTDMNATLLKI-DNRNI---VEYIKARTHLIRWVGLSRQKSNEVWKWEDG- 175
QY 148 ALSLSILSNSVVO-----KCGTIHRCGLHASSCEVALOWICEK 185
DB 176 ----SVISNMFEFLDGKNNMCAYFHNGKMHPTFCENKHYLMCER 218

RESULT 9
US-09-531-056A-6
Sequence 6, Application US/09531056A
Patent No. 6455683
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUS
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: DB20 NP
CURRENT APPLICATION NUMBER: US/09/531,056A
CURRENT FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 191
TYPE: PRT
ORGANISM: Homo sapiens
US-09-531-056A-6

Query Match 16.8%; Score 174.5; DB 4; Length 191;
Best Local Similarity 25.8%; Pred. No. 2.8e-11;
Matches 48; Conservative 29; Mismatches 84; Indels 25; Gaps 6;
QY 11 ELPAAPRVQDDSRWKVKAVLHRCPCVSYLVMAVGLLTVILMSLL--LYORTLCCGSKGPM 68
DB 15 ELPANPGCLHSKEHSIKATL-----IWLFFELIMFTIIVCGMVAALSIRANCHQPSV 69
QY 69 CSQCSCRCPLNWRNGSHCYFYSMEKRDWNSLKFCADKGSLLTTPDNQGVNLFQEVVGE 128
DB 70 CLQAA--CPESWIGFORKCFYFSDTKNWTSSORFCDSDQADLAQVESFQELNLLRYKGP 128
QY 129 DFYWIGLRDIDG--WRWEDG-----PALSLSILSNSVVKCGTIHRCGLHASSCEVAL 179
DB 129 SDHWIGLSREQQPMKWINGTWTROPFPLGAG-----ECAYLNDKGASSARHYTER 180

STATE: D.C.
COUNTRY: UNITED STATES OF AMERICA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,126A
FILING DATE: 08-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECHT=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-722-126A-8

Query Match 16.1%; Score 166.5; DB 3; Length 115;
Best Local Similarity 27.4%; Pred. No. 1.1e-10;
Matches 31; Conservative 22; Mismatches 57; Indels 3; Gaps 2;

QY 75 CPNLWMRNGSHCYFSEMEKRDWNSLSLKFCADKGSLLTFPDNQGYNLFQEVYVGEDFYWG 134
DB 1 CSEDWVGQRCYFISTVKRSWTSQAQNCSEHGATLAVIDSEKDNFLKRYAGREHWVG 60
QY 135 LRDIDG--WRWEDGPALSLSILSNVQKCGTIHRCGLHASSCEVALOWICEK 185
DB 61 LKKEGHPKWSNGKEFN-NWENVGSDKCVFLKNTVSSMECEKNLYWICNK 112

RESULT 13
PCT-US95-04258-8
Sequence 8, Application PC/TUS9504258
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
FUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: BROWDY AND NETMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994

ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECHT=1 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04258-8

Query Match 16.1%; Score 166.5; DB 5; Length 115;
Best Local Similarity 27.4%; Pred. No. 1.1e-10;
Matches 31; Conservative 22; Mismatches 57; Indels 3; Gaps 2;

QY 75 CPNLWMRNGSHCYFSEMEKRDWNSLSLKFCADKGSLLTFPDNQGYNLFQEVYVGEDFYWG 134
DB 1 CSEDWVGQRCYFISTVKRSWTSQAQNCSEHGATLAVIDSEKDNFLKRYAGREHWVG 60
QY 135 LRDIDG--WRWEDGPALSLSILSNVQKCGTIHRCGLHASSCEVALOWICEK 185
DB 61 LKKEGHPKWSNGKEFN-NWENVGSDKCVFLKNTVSSMECEKNLYWICNK 112

RESULT 14
US-09-127-946-14
Sequence 14, Application US/09127946
Patent No. 6416973
GENERAL INFORMATION:
APPLICANT: Bakker, Alexander B.H.
APPLICANT: Phillips, Joseph H.
APPLICANT: Lanier, Lewis L.
TITLE OF INVENTION: Mammalian Cell Membrane Proteins;
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,946
FILING DATE: 31-JUL-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/089,168
FILING DATE: 12-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/069,692
FILING DATE: 16-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/069,639
FILING DATE: 15-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/063,717
FILING DATE: 29-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/054,430
FILING DATE: 01-AUG-1997
ATTORNEY/AGENT INFORMATION:

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:30:38 ; Search time 17 Seconds
(without alignments)
1069.423 Million cell updates/sec

Title: US-09-811-367B-1
Perfect score: 1023
Sequence: 1 MTDSVIYSMLELPTAQON.....GLQASSCEVPLHGVCCKVRL 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 95820

Minimum DB seq length: 0
Maximum DB seq length: 189

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	ID	Description	
1	525.5	51.4	188	2 I59421	mast cell function	
2	166	16.2	156	2 T28141	C type lectin, B locus	
3	153.5	15.0	167	1 WMVZF2	hepatic lectin hom	
4	149	14.6	170	2 T28140	natural killer cel	
5	143.5	14.0	144	2 PC7027	aggratin alpha cha	
6	142	13.9	146	2 JC7135	agkisacutacin beta	
7	137.5	13.4	175	2 S29822	pancreatitits-assoc	
8	137	13.4	185	2 A28351	pancreatic stone p	
9	136	13.3	163	1 A34313	antifreeze protein	
10	135	13.2	146	2 JC7105	aggratin beta chai	
11	134.5	13.1	175	2 A37194	pancreatic thread	
12	132.5	13.0	175	2 A41719	pancreatic stone p	
13	130.5	12.8	175	2 A49616	pancreatitits-assoc	
14	129.5	12.7	162	1 LNRC3	lectin BRA3-2 prec	
15	128	12.5	146	2 JC4691	coagulation factor	
16	128	12.5	166	1 RGHU1B	regenerating islet	
17	123.5	12.1	133	2 A47267	botrocetin alpha c	
18	122.5	12.0	162	1 LNRC1	lectin BRA3-1 prec	
19	122	11.9	174	2 S54379	pancreatitits-assoc	
20	121.5	11.9	125	2 B47267	botrocetin beta ch	
21	120	11.7	123	2 JC2415	echicetin beta cha	
22	119.5	11.7	131	2 JC5058	bitiscetin alpha c	
23	119	11.6	129	2 JC4329	coagulation factor	
24	118.5	11.6	123	2 B42972	coagulation factor	
25	117	11.4	125	2 JC5059	bitiscetin beta ch	
26	116	11.3	155	2 S78774	perlucin - Halioti	
27	115	11.2	166	1 RGHU1A	regenerating islet	
28	113	11.0	166	2 A45751	pancreatic stone p	
29	111	10.9	174	2 I83377	regenerating prote	

ALIGNMENTS

RESULT 1

I59421
mast cell function associated antigen - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
R;Accession: I59421
R;Guthmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A;Title: A secretion inhibitory signal transduction molecule on mast cells is another C
A;Reference number: I59421; MUID:96016176; PMID:7568140
A;Accession: I59421
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-188 <RES>
A;Cross-references: EMBL:X79812; NID:g1020141; PIDN:CAA56208.1; PID:g1020142
C;Genetics:
A;Gene: mafa

Query Match 51.4%; Score 525.5; DB 2; Length 188;
Best Local Similarity 53.5%; Pred. No. 4.8e-42;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY	1	MTDSVIYSMLLELPTAQONDYGPQQKSSSSKPSCLVAITLGLTAVLLSVLLQWIL	60
Db	1	MADNSIYSTLELPAPAPRVQDDSKVKYAVLHRCVSYLVWVALGLLTIVLMSLLYQRTL	60
QY	61	COGSNYSTCASCPSCPDRAWKMGVHCYFVSVEKDNSSLEFCLARDSHLLVITDNOEMS	120
Db	61	CCGSKGFMCSQCSRCNLMWRNGSHCYFMSKRDWNSLKFCDKGSLLITFPDQGVN	120
QY	121	LLQVFUSEAFPCWITGLRNNSGWRWEDGSPINFSISSNFVQTGAINKNGLQASSCEVPL	180
Db	121	LFOEYVGEDFYWIGLIDIDGWRWEDGFALSLS-ILSNSVVKCGTTHRCGLHASSCEVAL	179
QY	181	HGVCKKV	187
Db	180	QWICEKV	186

RESULT 2

T28141
C type lectin, B locus - chicken
C:Species: Gallus gallus (chicken)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
R;Accession: T28141
R;Milne, S.; Kaufman, J.; Beck, S.
Submitted to the EMBL Data Library, May 1998
A;Description: DNA sequencing and analysis of the chicken major histocompatibility comp
A;Reference number: Z20475
A;Accession: T28141
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA

reg II, regenerati
reg I, regenerati
agkisacutacin alph
echinoidin - sea u
hepatic lectin hom
coagulation factor
pancreatitits-assoc
lectin - barnacle
ovocleidin - chick
A40R protein - vac
Salp2R protein pre
NK cell receptor h
hypothetical prote
type II antifreeze
hypothetical prote
hypothetical prote

A;Residues: 1-156 <MIL>
A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292545; PIDN:CAAL18961.1
A;Experimental source: clone cB12
C;Genetics:
A;Gene: Blec
A;Map position: 16
A;Introns: 17/1; 74/3; 110/2

Query Match 16.2%; Score 166; DB 2; Length 156;
Best Local Similarity 29.7%; Pred. No. 2.3e-08;
Matches 46; Conservative 19; Mismatches 69; Indels 22; Gaps 5;

Qy 42 TLGLTAVLLSVLYQWILCOGSNVTSCASPCSPDRWMKYGHCYFVSVEEKDWNSSLE 101
Db 6 TVLLITAVFAVQAFQ-----PHQPCAQCPFDWIGRGKCYFSEDESNTSSQN 56

Qy 102 FCLARDSHLLVITDQMSLLQVFLSEAFWCWIGLRNNS--GWRWEDGSPINFSRISNS 158
Db 57 NCSALGASLAVFDSAEDLSFTMRHKGSSPHWVGLSREGKEHPWVWNRSP-----SHL 110

Qy 159 F-VQ---TCGAINKNGLOASSCEVPLHGVCCKKVL 189
Db 111 PQVQDGLCAVLGDAGLSSSHCSTRNWNVCTKPAL 145

RESULT 3
WMVZF2
hepatitis B virus (BamHI-ORF2) - fowlpox virus (isolate HP-438 [Munich])
C;Species: fowlpox virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000
C;Accession: B29963
R;Tomley, F.; Binns, M.; Campbell, J.; Bournsnel, M.
J. Gen. Virol. 69, 1025-1040, 1988
A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpox virus
A;Reference number: J04442; MUID:88229622; PMID:2836548
A;Accession: B29963
A;Molecule type: DNA
A;Residues: 1-167 <TOM>
A;Cross-references: GB:D00295; NID:g221380; PIDN:BAA00192.1; PID:g221383
C;Superfamily: fowlpox virus hepatitis B virus
C;Keywords: early protein
F;49-152/Domain: C-type lectin homology <LCH>

Query Match 15.0%; Score 153.5; DB 1; Length 167;
Best Local Similarity 25.8%; Pred. No. 3.7e-07;
Matches 39; Conservative 29; Mismatches 74; Indels 9; Gaps 5;

Qy 36 SCLVAITGLTAVLLSVLYQWILCOGSNVTSCASPCSPDRWMKYGHCYFVSVEKD 95
Db 13 SCVAITVLGILCLILFTLVV--VTCW-VYAFYPYFVKVCPDEWIGYNSKCYFTINETN 69

Qy 96 WNSLSEFLCLARDSHLLVITDQMSLLQVFLSEAFWCWIGLRNNSGWRWEDGSPINFSRIS 155
Db 70 WNSKGLCDVMDSSLIRPDNITLNFVSRYGKGSY-WIDINQN---RKIPG--INFSLYY 123

Qy 156 SNSFVQTCGAINKNGLOASSCEVPLHGVCCK 186
Db 124 EQGVNDICLLFDTSNIHMSCLIFHERITCVK 154

RESULT 4
T28140
natural killer cell receptor homolog - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T28140
R;Milne, S.; Kaufman, J.; Beck, S.
submitted to the EMBL Data Library, May 1998
A;Description: DNA sequencing and analysis of the chicken major histocompatibility complex
A;Reference number: Z20475
A;Accession: T28140
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA

A;Residues: 1-170 <MIL>
A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292544; PIDN:CAAL18960.1
A;Experimental source: clone cB12
C;Genetics:
A;Gene: B-NK
A;Map position: 16
A;Note: Intron positions not resolved (incomplete sequence)

Query Match 14.6%; Score 149; DB 2; Length 170;
Best Local Similarity 28.6%; Pred. No. 9.9e-07;
Matches 34; Conservative 16; Mismatches 67; Indels 2; Gaps 2;

Qy 70 ASCPSCPDPRWMKYGHCYFVSVEEKDWNSSLEFLCLARDSHLLVITDQMSLLQVFLSEA 129
Db 45 AACLLCHQFVWLLGDRCYELSTEGKNWTQAKKCNLSQSLAVLRKKAEEHDLQOMAGAE 104

Qy 130 FCWIGLR-NNSGWRWEDGSPINFSRISNSFVQT-CGAINKNGLOASSCEVPLHGVCCK 186
Db 105 PVWIGLEVSTNQWKEVDNSSYNSTESDNLVSMENRCGTFKNTKVEGDVCSGHEQWVCOK 163

RESULT 5
PC7027
aggrexin alpha chain - Malayan pit viper (fragment)
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C;Accession: PC7027
R;Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A;Title: Molecular cloning and sequence analysis of aggrexin, a collagen-like platelet
A;Reference number: PC7027; MUID:59443731; PMID:10512747
A;Accession: PC7027
A;Molecule type: mRNA
A;Residues: 1-144 <CHU>
A;Experimental source: venom gland
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; platelet aggregation; venom

Query Match 14.0%; Score 143.5; DB 2; Length 144;
Best Local Similarity 29.6%; Pred. No. 2.7e-06;
Matches 34; Conservative 17; Mismatches 49; Indels 15; Gaps 4;

Qy 68 TCASPCSPDRWMKYGHCYFVSVEEKDWNSSLEFLCLARD--SHLLVITDQMSLLQVF 125
Db 6 TRAGLEDCDFGSPYDQHCYQAFNEQKTWDEAEKFCRAQENGHAHASTESNGEADFVSWL 65

Qy 126 LS-----EAFCWIGLR-----NNSGWRWEDGSPINFSRISNSFVQTCGAINK 168
Db 66 ISQKDELADEYVWIGLRQAKNQKQCSSEWSGSSVSYENL-IDLHTKKCGALEK 119

RESULT 6
JC7135
agkisacutacin beta chain precursor - sharp-nosed viper
N;Alternate names: fibrinogenolytic venom protein
C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000
C;Accession: JC7135; PC7038
R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
Biochem. Biophys. Res. Commun. 265, 530-535, 1999
A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenolytic veno
A;Reference number: JC7134; MUID:20025379; PMID:10558903
A;Accession: JC7135
A;Molecule type: mRNA
A;Residues: 1-146 <CHE>
A;Cross-references: GB:AF176421
A;Experimental source: venom gland
A;Accession: PC7038
A;Molecule type: protein
A;Residues: 24-50;59-83;102-107;112-114 <CH2>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-146/Product: egkiascutacin beta chain #status experimental <MAT>

Query Match 13.9%; Score 142; DB 2; Length 146;
Best Local Similarity 25.0%; Pred. No. 3.9e-06;
Matches 42; Conservative 21; Mismatches 55; Indels 50; Gaps 8;

QY 39 VAITGLTAVLLVLLVYLWILCOGNSYTCASCPCPRRMKYNHCYFVSVEKDWN 98

Db 5 IFVSGLLVVFL-----SLSGPAADCPSEWSSYEGHCYKPFDEPKTWAD 48

QY 99 SLEFCLAA--RDShLLVITDNOE-----MSLLQVFLSEAFQWIGLR---NNSGWRWEDGSP 149

Db 49 AEKFCCTQKHGSHLAFHSSEADFVTLTPSLKTLVWIGLKNWGCYKWSGDKL 108

QY 150 NF-----SRISNSFV--QTCAINKNGLQASCEVPLHGVC 185

Db 109 DYKDWREQFECLVSRVTNNWLSMDCG-----TTCSEF-----VCK 143

RESULT 7

S29822

pancreatitis-associated protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000

C:Accession: S29822

R:Ittoh, T.; Teraoka, H.

A:Biotech. Biophys. Acta 1172, 184-186, 1993

A:Title: Cloning and tissue-specific expression of cDNAs for the human and mouse homolog

A:Reference number: S29821; MUID:93176807; PMID:7679928

A:Accession: S29822

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-175 <I>O>

A:Cross-references: GB:D13509; NID:g286106; PIDN:BAA02727.1; PID:g286107

C:Superfamily: tetranectin; C-type lectin homology

F;40-171/Domain: C-type lectin homology <LCH>

Query Match 13.4%; Score 137.5; DB 2; Length 175;

Best Local Similarity 25.7%; Pred. No. 1.2e-05;

Matches 46; Conservative 28; Mismatches 70; Indels 35; Gaps 9;

QY 33 PSCSLVAITLGLTAVLLVLLVYLWILCOGNSYTCASCPCP-----SCPDRMKYGNHCY 88

Db 3 PPTACSV-----MSWLLSLCLM---LLSQVQEDSLKNIPSAISCPKGSQAYGICYA 53

QY 89 FSVEEKDNSSLEFCLAR-DSHLLVITDNOEMLLQVFL-----SFAFCWIGLR----- 136

Db 54 LFQIPQTFDAELACQKRPQGHVLVLSNSAEASFLSMVKRTGNSYQYTWIGLHDPTLGA 113

QY 137 --NNSGWRWEDGSPNFPSRISSNSFVQT-----CGAINK-NGL---QASCEVPLHGVC 185

Db 114 BPNGGGEWNSNDVMVNFNWRNPSTALDRAFCGLSRASGFLKWRDTCVKLPYVCK 172

RESULT 8

A28351

pancreatic stone protein precursor - rat

N:Alternate names: lithostathine

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-May-2000

C:Accession: A28351; A39081; PLO147; S34618

R:Terazono, K.; Yamamoto, H.; Takasawa, S.; Shiga, K.; Yonemura, Y.; Tochino, Y.; Okamoto

J. Biol. Chem. 263, 2111-2114, 1988

A:Title: A novel gene activated in regenerating islets.

A:Reference number: A92704; MUID:88115343; PMID:2963000

A:Accession: A28351

A:Molecule type: mRNA

A:Residues: 1-165 <TER>

A:Cross-references: GB:M18962; NID:g206604; PIDN:AAA42028.1; PID:g206605

R:Rouquier, S.; Verdier, J.M.; Iovanna, J.; Dagorn, J.C.; Giorgi, D.

J. Biol. Chem. 266, 786-791, 1991

A:Title: Rat pancreatic stone protein messenger RNA. Abundant expression in mature exocrine

A:Reference number: A39081; MUID:91033273; PMID:1985964

A:Accession: A39081

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-165 <ROU>

A:Cross-references: GB:M62930; NID:g206462; PIDN:AAA41974.1; PID:g206463

R:Adrich, Z.; De Caro, A.M.; Guidoni, A.A.; Woudstra, M.E.; Rovey, M.

Comp. Biochem. Physiol. B 93, 793-797, 1989

A:Title: Characterization in rat pancreatic juice of a protein homologous to the human I

A:Reference number: PLO147; MUID:90031455; PMID:2680252

A:Accession: PLO147

A:Molecule type: protein

A:Residues: 22-69 <ADR>

A:Experimental source: pancreas

R:Dusetti, N.J.; Frigerio, J.M.; Dagorn, J.C.; Iovanna, J.L.

Biochim. Biophys. Acta 1174, 99-102, 1993

A:Title: Rapid PCR cloning and sequence determination of the rat lithostathine gene.

A:Reference number: S34618; MUID:93326645; PMID:7916640

A:Accession: S34618

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-165 <DUS>

A:Cross-references: EMBL:L07512; NID:g393208; PIDN:AAA41533.1; PID:g393209

C:Comment: This protein is found in pancreatic calculi of mammals. A peptide bond between

rocin into an insoluble protein at a neutral pH of 5.5 to 7.5.

C:Genetics: 21/1; 60/3; 106/3; 144/1

C:Superfamily: tetranectin; C-type lectin homology

C:Keywords: pyrrolutamic acid

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-165/Product: pancreatic stone protein #status predicted <MAT>

F;35-161/Domain: C-type lectin homology <LCH>

F;22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimer

Query Match 13.4%; Score 137; DB 2; Length 165;

Best Local Similarity 27.2%; Pred. No. 1.3e-05;

Matches 43; Conservative 23; Mismatches 68; Indels 24; Gaps 7;

QY 49 VLLSVLLVYLWILCOGNSYTCASCPCP-----CPDRMKYGNHCYFVSVEKDWNSSLEFCL 104

Db 8 ILLSLCLM---VLSPSQGEAEEDLPSARITCEGNSAYSSCYFYFMEHLNSWAEDLFCQ 64

QY 105 ARDS-HLLVITDNOEMLLQVFLSE-----AFCWIGL---RNSGWRWEDGSPNLF--- 151

Db 65 NNSGVLVSVLSQAEGNFLASLIKSGTTAANNVWIGLHDPKNNRRWHWSGSLFLYKSWD 124

QY 152 SRISNSFVQTCAINKNG-----LQASCEVPLHGVC 185

Db 125 TGYPNNSNGYCVSVTSNSGYKKWRDNSCDAQLSFVCK 162

RESULT 9

A34313

antifreeze protein II precursor - sea raven

N:Alternate names: pro-antifreeze protein type II

C:Species: Hemitripterus americanus (sea raven)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A34313; A24602; PC2386; PC2387; S65733

R:Hayes, P.H.; Scott, G.K.; Ng, N.F.L.; Hew, C.L.; Davies, P.L.

J. Biol. Chem. 264, 18761-18767, 1989

A:Title: Cystine-rich type II antifreeze protein precursor is initiated from the third .

A:Reference number: A34313; MUID:90036986; PMID:2572595

A:Accession: A34313

A:Molecule type: DNA; mRNA

A:Residues: 1-37, 'G', 39-163 <HAY>

A:Cross-references: GB:J05100; NID:g213875; PIDN:AAA49618.1; PID:g213876

A:Note: there are 12-15 copies in the genome; the sequence of SR7 was determined

A:Note: the initiator codon was determined

A:Note: parts of this sequence, including the amino end of the mature protein, were det

A:Note: the amino end of the mature protein is blocked

R:Ng, N.F.; Trinh, K.Y.; Hew, C.L.

J. Biol. Chem. 261, 15690-15695, 1986

A:Title: Structure of an antifreeze polypeptide precursor from the sea raven, Hemitript

A:Reference number: A24602; MUID:87057207; PMID:3782083

A;Accession: A24602
A;Molecule type: mRNA
A;Residues: 'MORQADTETREDISTAGLSIIIVCTISTTTR' 1-163 <NGN>
A;Cross-references: GB:J02593; NID:G213873; PIDN:AAA49617.1; PID:G213874
A;Note: parts of this sequence were determined by protein sequencing
R;Dunker, B.P.; Gauthier, S.Y.; Davies, P.L.
Biochem. Biophys. Res. Commun. 203, 1851-1857, 1994
A;Title: Cystine-rich fish antifreeze is produced as an active proprotein precursor in f
A;Reference number: PC2386; MUID:95032070; PMID:7945337
A;Accession: PC2386
A;Molecule type: mRNA
A;Residues: 1-45 <DUM>
A;Accession: PC2387
A;Molecule type: protein
A;Residues: 18-27 <DU2>
R;Dunker, B.P.; Gauthier, S.Y.; Davies, P.L.
Biochim. Biophys. Acta 1292, 312-316, 1996
A;Title: Evidence for a proprotein intermediate during maturation of type II antifreeze
A;Reference number: S65733; MUID:96176860; PMID:8597578
A;Accession: S65733
A;Molecule type: protein
A;Residues: 18-22 <DUW>
C;Genetics:
A;Insertions: 21/1; 66/3; 105/3; 142/1
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: pyroglutamic acid
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-34/Domain: propeptide #status experimental <PRO>
F;35-163/Product: antifreeze protein 11 #status predicted <MAT>
F;41-159/Domain: C-type lectin homology <LCH>
F;41-Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
F;41-52,69-159,135-151/Disulfide bonds: #status predicted
Query Match 13.3%; Score 136; DB 1; Length 163;
Best Local Similarity 31.7%; Pred. No. 1.6e-05;
Matches 26; Conservative 10; Mismatches 42; Indels 4; Gaps 2;
Qy 73 PSCDRWMKYGNHCYFVSVEEKDNSSLEFCLARDSHLLVITDQMSLLQVFLSEAFWC 132
Db 39 ENCPAGQPLGDCIYYETTAMTALARTNCMLGGLASHSQEHSFIQT-LNAGVW 97
Qy 133 IG---LRNSGRWEDGSPLNF 151
Db 98 IGGSAQLQAGAWTWSGDTPMNF 119
RESULT 10
JC7105
aggreitin beta chain - Malayan pit viper
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C;Accession: JC7105
R;Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A;Title: Molecular cloning and sequence analysis of aggreitin, a collagen-like platelet a
A;Reference number: PC7027; MUID:99443731; PMID:10512747
A;Accession: JC7105
A;Molecule type: mRNA
A;Residues: 1-146 <CHU>
A;Experimental source: venom gland
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; platelet aggregation; venom
Query Match 13.2%; Score 135; DB 2; Length 146;
Best Local Similarity 25.2%; Pred. No. 1.8e-05;
Matches 40; Conservative 19; Mismatches 58; Indels 32; Gaps 6;
Qy 39 VAITLGLTAVLLSVLLVQWILCOGSNYSTACSPCDRWMKYGNHCYFVSVEEKDWS 98
Db 5 IFVSGFLVAVFL-----SLSGTGADCPSGWSSYEGHCYKPFNEPKNWAD 48
Qy 99 SLRFCL-LARDSHLLVITDQNE---MSLLQVFLSEAFWCWIGLEN---NSGRWEDGSPL 149

Db 49 AERFCKLQPKHSHLVFSQSAEADFVVKLTRPRLKANLVMMGLSNWGHGNCWQWSDGARL 108
Qy 150 NFSRISSNSFVOTCGAINKNGLO---ASSCEVPLHGVC 185
Db 109 NYKDWQSQECLAPRGVHTWLNMDSCSTCSF-----VCK 143
RESULT 11
A37194
pancreatic thread protein precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 20-Aug-1999
C;Accession: A37194; A53897
R;de la Monte, S.M.; Ozturk, M.; Wands, J.R.
J. Clin. Invest. 86, 1004-1013, 1990
A;Title: Enhanced expression of an exocrine pancreatic protein in Alzheimer's disease a
A;Reference number: A37194; MUID:90368981; PMID:2394826
A;Accession: A37194
A;Molecule type: mRNA
A;Residues: 1-175
A;Cross-references: GB:M59794; NID:G163648; PIDN:AAA30750.1; PID:G163649
R;Cai, L.; Harris, W.R.; Marshak, D.R.; Gross, J.; Crabb, J.W.
J. Protein Chem. 9, 623-632, 1990
A;Title: Structural analysis of bovine pancreatic thread protein.
A;Reference number: A53897; MUID:91197388; PMID:2085387
A;Accession: A53897
A;Molecule type: protein
A;Residues: 38-138;141-175 <CAI>
C;Comment: The purified protein undergoes a reversible globule-fibril transformation an
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; extracellular protein; pancreas
F;38-138/Product: pancreatic thread protein chain A #status experimental <ACH>
F;40-171/Domain: C-type lectin homology <LCH>
F;141-175/Product: pancreatic thread protein chain B #status experimental <BCH>
Query Match 13.1%; Score 134.5; DB 2; Length 175;
Best Local Similarity 27.4%; Pred. No. 2.3e-05;
Matches 48; Conservative 27; Mismatches 63; Indels 37; Gaps 9;
Qy 42 TLGI--LTAVLLSVLLVQWILCOGSNYSTCASCP---SCPDRWMKYGNHCYFVSVEEKD 95
Db 4 SLGLPRLSWMLLSCLM---LLSQIQGENSKPELSARISCPSGSMAYRSHCYALFKTPKT 60
Qy 96 WNSLEFCLARDS-HLLVITDQNEMSLLQVFL-----SEAFWCWIGLR-----NNSGW 141
Db 61 WMDADIACQKPSGHLVSLSGAESFVASIVRNLTQSDIWLGLHDPTGSEANAGW 120
Qy 142 RWEDGSPLNF-----SRISNSFVOTCGAINKNG---LQASSCEVPLHGVC 185
Db 121 EWISNDVLNVAVETDPAALSSPGY---CGSLRSRGYLKWRDHNCNINLPYVCK 172
RESULT 12
A41719
pancreatic stone protein 2 precursor - rat
N;Alternate names: pancreatitis-associated protein; regenerating protein 2
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 20-Jun-2000
C;Accession: A37456; A59313; I51899; JC1257; A41719
R;Dusetti, N.J.; Frigerio, J.M.; Keim, V.; Dagorn, J.C.; Iovanna, J.L.
J. Biol. Chem. 268, 14470-14475, 1993
A;Title: Structural organization of the gene encoding the rat pancreatitis-associated p
on domain-containing genes.
A;Reference number: A37456; MUID:93300847; PMID:8314803
A;Accession: A37456
A;Molecule type: DNA
A;Residues: 1-175 <DUS1>
A;Cross-references: GB:L07127; NID:G349550
A;Experimental source: strain Wistar; tissue type liver
A;Note: only intron/exon boundaries are shown; exon I and the beginning of exon II are
ension of the open reading frame to an ATG codon in exon I is shown in accession A59313
R;Dusetti, N.J.; Frigerio, J.M.; Keim, V.; Dagorn, J.C.; Iovanna, J.L.
submitted to GenBank, August 1993

A;Reference number: A59313
A;Accession: A59313
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-175 <DUS2>
A;Cross-references: GB:107127; NID:G349550; PIDN:AAA41805.1; PID:G349551
A;Note: an incorrect initiation codon was used
R;Iovanna, J.L.; Keim, V.; Bosshard, A.; Orelle, B.; Frigerio, J.M.; Duseti, N.; Dagorn
Am J. Physiol. 265, G611-6618, 1993
A;Title: FAP, a pancreatic secretory protein induced during acute pancreatitis, is expressed in the rat pancreas
A;Reference number: I51899; MUID:94056762; PMID:8238345
A;Accession: I51899
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-175 <IOV1>
A;Cross-references: GB:M98049; NID:G393210; PIDN:AAA16341.1; PID:G393211
A;Note: in Genbank entry R4PAPC, release 113.0, the source is designated as Rattus rattus
R;Kaminura, T.; West, C.; Beutler, E.
Gene 118, 299-300, 1992
A;Title: Sequence of a cDNA clone encoding a rat Reg-2 protein.
A;Reference number: JCI257; MUID:92380521; PMID:1511905
A;Accession: JCI257
A;Molecule type: mRNA
A;Residues: 1-6, 'S', 'B'-175 <KAM>
A;Cross-references: GB:843715; NID:G254694; PIDN:AAAB23103.1; PID:G254695
R;Iovanna, J.; Orelle, B.; Keim, V.; Dagorn, J.C.
J. Biol. Chem. 266, 24664-24669, 1991
A;Title: Messenger RNA sequence and expression of rat pancreatitis-associated protein, a novel protein
A;Reference number: A41719; MUID:92105133; PMID:1722211
A;Accession: A41719
A;Molecule type: mRNA
A;Residues: 1-175 <IOV2>
A;Cross-references: GB:M55149; NID:G206030; PIDN:AAA41807.1; PID:G206031
A;Note: the amino-terminal residue of the mature protein was identified as Glu
C;Genetics:
A;Gene: pap
A;Introns: 26/1; 65/3; 111/3; 154/1
A;Note: the first intron occurs before the initiator codon
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: lectin; pancreas
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-175/Product: pancreatitis-associated protein #status experimental <MAT>
F;40-171/Domain: C-type lectin homology <LCH>
F;40-51,68-171,146-163/Disulfide bonds: #status predicted

Query Match 13.0%; Score 132.5; DB 2; Length 175;
Best Local Similarity 25.4%; Pred. No. 3.6e-05;
Matches 42; Conservative 28; Mismatches 68; Indels 29; Gaps 7;
QY 45 LLTAVLLVLLYQWILCOGNSYTCASCP-----SCPDRWKYGNHCYFVSVEKDWNSL 100
Db 9 VMSWMLLSCLM---LISVQGESEPKIPARISCPSQAYGSCYALFQIPCTWFDAAE 65
QY 101 EFCILAR-DSHLVITDQEMSLQVFL-----SEAFCWIGLR-----NNSGWRWEDG 146
Db 66 LAQKPEGHVSLVNAEASFSLAMVKNYQYTWICLHPTLGGRNGGWSNN 125
QY 147 SPINFRISNSVQT-----CGAINKNG-----IQASCEVPLHGVCCK 185
Db 126 DIMNYVWERNPSTALDRGFCGSLRSGFLRWDRITTCVKLPYVCK 172

RESULT 13
A49616
pancreatitis-associated protein precursor - human
N;Alternate names: C-type lectin; pancreatic human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 21-Jul-2000
C;Accession: A49616; A44931; S29821; S48197; I55580
R;Duseti, N.J.; Frigerio, J.M.; Fox, M.F.; Swallow, D.M.; Dagorn, J.C.; Iovanna, J.L.
Genomics 19, 108-114, 1994
A;Title: Molecular cloning, genomic organization, and chromosomal localization of the human BRA3-2 precursor - barnacle (Megabalanus rosa)
A;Reference number: A49616; MUID:94245143; PMID:8188210

A;Accession: A49616
A;Molecule type: DNA
A;Residues: 1-175 <DUS>
A;Cross-references: GB:115533; NID:G482308; PIDN:AAA60020.1; PID:G482309
R;Lasserre, C.; Christa, L.; Simon, M.T.; Vernier, P.; Brechot, C.
Cancer Res. 52, 5089-5095, 1992
A;Title: A novel gene (HIP) activated in human primary liver cancer.
A;Reference number: A44931; MUID:92386513; PMID:1325291
A;Accession: A44931
A;Molecule type: mRNA
A;Residues: 1-175 <LAS>
A;Cross-references: GB:X68641; NID:G312806; PIDN:CAA48605.1; PID:G312807
A;Experimental source: hepatocellular carcinoma
A;Note: sequence extracted from NCBI backbone (NCBIN:113007, NCBIP:113008)
Biochim. Biophys. Acta 1172, 184-186, 1993
A;Title: Cloning and tissue-specific expression of cDNAs for the human and mouse homologs of the rat protein
A;Reference number: S29821; MUID:93176807; PMID:7679928
A;Accession: S29821
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-175 <ITO>
A;Cross-references: GB:D13510; NID:G285970; PIDN:BAA02728.1; PID:G285971
R;Lasserre, C.; Simon, M.T.; Ishikawa, H.; Diriong, S.; Nguyen, V.C.; Christa, L.; Vernier, J.
Eur. J. Biochem. 224, 29-38, 1994
A;Title: Structural organization and chromosomal localization of a human gene (HIP/PAP)
A;Reference number: S48197; MUID:94357229; PMID:8076648
A;Accession: S48197
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-175 <LA2>
R;Orelle, B.; Keim, V.; Masciotra, L.; Dagorn, J.C.; Iovanna, J.L.
J. Clin. Invest. 90, 2284-2291, 1992
A;Title: Human pancreatitis-associated protein. Messenger RNA cloning and expression in transgenic mice
A;Reference number: I55580; MUID:93107309; PMID:1469087
A;Accession: I55580
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-175 <RES>
A;Cross-references: GB:S51768; NID:G262368; PIDN:AAAB24642.1; PID:G262369
C;Genetics:
A;Gene: GDB:PAP; HIP
A;Cross-references: GDB:136839; OMIM:167805
A;Map position: 2p12-2p12
A;Introns: 26/1; 65/3; 111/3; 154/1
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: acute phase; extracellular protein; pancreas
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-175/Product: pancreatitis-associated protein #status predicted <MAT>
F;40-171/Domain: C-type lectin homology <LCH>
F;40-51,68-171,146-163/Disulfide bonds: #status predicted

Query Match 12.8%; Score 130.5; DB 2; Length 175;
Best Local Similarity 26.0%; Pred. No. 5.6e-05;
Matches 46; Conservative 25; Mismatches 71; Indels 35; Gaps 8;
QY 38 LVAITGLTAVLLSVLLYQWILCOGNSYTCASCP-----CPDRWKYGNHCYFVSVEE 93
Db 2 LPPMALPSVSWMLLSCLM---LISVQGESEPKIPARISCPSQAYGSCYALFQIPCTWFDAAE 58
QY 94 KDNWSSLEFCLARDS-HLLVITDQEMSLQVFL-----SEAFCWIGLR-----NNS 139
Db 59 KSWTDADLACQRRPSGNLVSLGAEQSVSLVSKISGNSYSYVWVIGLHDPQTGGTFPGE 118
QY 140 GWRWEDGSLNF-----SRISNSFVQTCAINKNGL-----QASSCVEPLHGVCCK 185
Db 119 GWEWSSDVMYFAWERNFTISSPGH---CASLSRSTAFLEKWDYCNVRLPYVCK 172

RESULT 14
LNRC3
lectin BRA3-2 precursor - barnacle (Megabalanus rosa)
C;Species: Megabalanus rosa

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:20:38 ; Search time 13 Seconds

(without alignments)
757.020 Million cell updates/sec

Title: US-09-811-367B-1

Perfect score: 1023

Sequence: 1 WTDSVIYSMLPLTATQON.....GLQASCEVPLHGVCCKVRL 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 41282

Minimum DB seq length: 0

Maximum DB seq length: 189

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198.5	19.4	179	1 CD94 MACMU	Q9mzk9 macaca mla
2	196.5	19.2	179	1 CD94 HUMAN	Q13241 homo sapien
3	194.5	19.0	179	1 CD94_PANTR	Q9mz41 pan troglod
4	1175	17.1	149	1 CLE2_HUMAN	Q92478 homo sapien
5	156.5	15.3	163	1 V239_FOWPV	P14371 fowipox vir
6	153.5	15.0	167	1 V008_FOWPV	P14370 fowipox vir
7	147.5	14.4	175	1 PBCG_MESAU	Q92778 mesocricetu
8	147	14.4	174	1 PAP3_MOUSE	O09049 mus musculu
9	146	14.3	117	1 CHBB_CROHO	P81509 crocalus ho
10	137.5	13.4	175	1 PAP1_MOUSE	P35230 mus musculu
11	137	13.4	165	1 LITH_RAT	P10758 rattus norv
12	136	13.3	163	1 ANP_HEMAM	P05140 hemitriptier
13	134.5	13.1	175	1 LITH_BOVIN	P23132 bos taurus
14	134.5	13.1	175	1 PAP2_MOUSE	O09037 mus musculu
15	134	13.1	146	1 MMHB_AKHA	Q9yi92 agkistrodon
16	132.5	13.0	175	1 PAP1_RAT	P25031 rattus norv
17	132	12.9	148	1 CVXB_CRODU	Q93427 crocalus du
18	130.5	12.8	175	1 PAP1_HUMAN	Q06141 homo sapien
19	129.5	12.7	162	1 LEC3_MEGRO	P07439 megabalanus
20	128	12.5	146	1 IXB_TRIFL	P23807 trimeresuru
21	128	12.5	166	1 LITB_HUMAN	P48304 homo sapien
22	126	12.3	133	1 RHCA_AGRKH	P81397 agkistrodon
23	124	12.1	123	1 ABAA_TRIAB	P81114 trimeresuru
24	123.5	12.1	133	1 BOTA_BOTJA	P22029 bothrops ja
25	123	12.0	131	1 ABAT_TRIAB	P81111 trimeresuru
26	123	12.0	155	1 PLC_HALLA	P82596 hallotis la
27	123	12.0	158	1 CVXA_CRODU	Q93426 crocalus du
28	122	11.9	174	1 PAP3_RAT	P42854 rattus norv
29	121.5	11.9	125	1 BOTB_BOTJA	P22030 bothrops ja
30	120	11.7	123	1 ECHB_ECHCA	P81996 echis carin
31	115	11.2	134	1 ABAT_TRIAB	P81112 trimeresuru
32	115	11.2	166	1 LITA_HUMAN	P05451 homo sapien
33	113.5	11.1	158	1 NKGF_PANTR	Q95m11 pan troglod

RESULT 1

ID	CD94_MACMU	STANDARD;	PRT;	179 AA.
AC	Q9MZX9; Q9GK91; Q9MZX7; Q9MZX8;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Natural killer cells antigen CD94 (NK cell receptor) (Killer cell			
DE	lectin-like receptor subfamily D, member 1).			
GN	KLRD1 OR CD94.			
OS	Macaca mulatta (Rhesus macaque).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;			
OC	Cercopitheidae; Macaca.			
OX	NCBI_TaxID=9544;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).			
RX	MEDLINE=20322487; PubMed=10866118;			
RA	LaBonte M.L., Levy D.B., Letvin N.L.;			
RT	"Characterization of rhesus monkey CD94/NKG2 family members and			
RT	identification of novel transmembrane-deleted forms of NKG2-A, B, C,			
RT	and D.";			
RL	Immunogenetics 51:496-499(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=21158386; PubMed=11261935;			
RA	Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.;			
RT	"Selective expression of NKG2-A and NKG2-C mRNAs and novel alternative			
RT	splicing of 5' exons in rhesus monkey decidua.";			
RL	Immunogenetics 53:69-73(2001).			
CC	-!- FUNCTION: Plays a role as a receptor for the recognition of MHC			
CC	class I HLA-E molecules by NK cells and some cytotoxic T-cells.			
CC	-!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family			
CC	members.			
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein.			
CC	-!- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=3;			
CC	Name=1; Synonyms=CD94-A;			
CC	isoId=Q9MZX9-1; Sequence=Displayed;			
CC	Name=2; Synonyms=CD94-B;			
CC	isoId=Q9MZX9-2; Sequence=VSP_003055;			
CC	Name=3; Synonyms=CD94 alt;			
CC	isoId=Q9MZX9-3; Sequence=VSP_003054;			
CC	-!- TISSUE SPECIFICITY: Natural killer cells.			
CC	-!- SIMILARITY: Contains 1 C-type lectin family domain.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF190931; AAF74527.1; -.			
DR	EMBL; AF190932; AAF74528.1; -.			

ALIGNMENTS

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DR EMBL; AF190933; AAF74529.1; -.
DR EMBL; AF294886; AAG34498.1; -.
DR HSP; P22897; LEGG.
DR InterPro; IPR001304; Lectin C.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS00411; C-TYPE LECTIN 2; 1.
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing; Polymorphism.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 89 174 BY SIMILARITY.
FT DISULFID 152 166 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPLIC 1 34 MAVKKTLLRLISGTGLIICLSMATLGLLKNS -> MAA
(in isoform 3).
FT FTid=VSP_003054.
FT L -> LQ (in isoform 2).
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FT Y -> D.
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Query Match 19.4%; Score 198.5; DB 1; Length 179;
Best Local Similarity 33.3%; Pred. No. 5.6e-12;
Matches 54; Conservative 24; Mismatches 69; Indels 15; Gaps 7;
QY 35 CSQLVAITGLTAVLLSVLLYQWLLCOGSN--YSTCASCPCSPDRMMKGNHCYFSVE 92
DB 20 CLSLMA-TLGLLLKNSFKLVSEYPPGPNIEIQKSDCCSCHEKMGVPCNCFISSE 78
QY 93 EKWNSSLEFCIARDSHLLVITDQEMSLQVFLSEAFCTWGL---RNNSGRWEDGSPL 149
DB 79 EKTWNESRHFCQSKSSLLQNRDELDFMS--SSQHFYWLGLSYSEHTAWLWENGSA 136
QY 150 NFRSISNSP-----VQTCGALKNG-LQASCEVPLHGVCVK 186
DB 137 --SQYLPFSFTFPKNCIAYNSGNALDESCETKNRYICKQ 176

RESULT 2
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ID CD94_HUMAN STANDARD; PRT; 179 AA.
AC Q13241; O43321; O43773; Q9UBB3; Q9UEQ0;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
lectin-like receptor subfamily D, member 1) (KP43).
GN KLRL1 OR CD94.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=96011848; PubMed=7589107;
RA Chang C., Rodriguez A., Carretero M., Lopez-Botet M., Phillips J.H.,
RA Lanier L.L.;
FT "Molecular characterization of human CD94: a type II membrane
glycoprotein related to the C-type lectin superfamily.";
Eur. J. Immunol. 25:2433-2437(1995).
[2]
SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=98139529; PubMed=9472066;
RA Rodriguez A., Carretero M., Glienke J., Bellon T., Ramirez A.,

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RA Lebrach H., Francis P., Lopez-Botet M.;
RT "Structure of the human CD94 C-Type lectin gene.";
RL Immunogenetics 47:305-309(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Biassoni R.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=98267245; PubMed=9601951;
RA Furukawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T., Tadokoro K.,
RA Tohma S., Inoue T., Yamamoto K., Juji T.;
RT "A alternatively spliced form of the human CD94 gene.";
RN Immunogenetics 48:87-88(1998).
[5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RT TISSUE=Blood;
RX MEDLINE=92388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield A., Schein J.B., Jones S.J.M., Skalska U., Smaluk D.B.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
members.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=1; Synonyms=CD94-A;
IsoId=Q13241-1; Sequence=Displayed;
Name=2; Synonyms=CD94-B;
IsoId=Q13241-2; Sequence=VSP_003053;
Name=3; Synonyms=CD94 alt;
IsoId=Q13241-3; Sequence=VSP_003052;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD94 entry;
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd94.htm".
-----
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EMBL; U30610; AAC50291.1; -.
DR EMBL; Y14287; CAA74663.1; -.
DR EMBL; Y14288; CAA74663.1; JOINED.
DR EMBL; AJ000673; CAA04230.1; -.
DR EMBL; AJ000001; CAA03845.1; -.
DR EMBL; AB009597; BAA24450.1; -.
DR EMBL; AB010084; BAA24451.1; -.
DR EMBL; BC028009; AAH28009.1; -.
DR PDB; 1B6E; 15-JUN-99.

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DR Genew; HGNC:6378; KLRD1.
DR MIM; 602894; -.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0004888; P:transmembrane receptor activity; TAS.
DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing; 3D-structure.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 89 174 BY SIMILARITY.
FT DISULFID 152 166 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 34 MAVFTTLWRLISGTLGIICLSIMATLIGLLKNS -> MAA
(in isoform 3).
FT VARSPLIC 105 105 /FTId=VSP 003052.
FT VARSPLIC 105 105 L -> LQ (in isoform 2).
FT VARSPLIC 105 105 /FTId=VSP 003053.
SQ SEQUENCE 179 AA; 20497 MW; 1884D99E8D9583A7 CRC64;
Query Match 19.2%; Score 196.5; DB 1; Length 179;
Best Local Similarity 32.7%; Pred. No. 8.6e-12;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;
QY 35 CSCLVAITLGLTAVLLSVLLYQWILCOGSN--YSTCASCPCSPDRMMKYGNHCYFVSVE 92
DB 20 CLSLMA-TLIGLLKNSFTKLSIEPAFTPGFNLELQKSDCCSCQKWKVGRNCYFISSE 78
QY 93 EKDWSSLEFFCLARDSHLIVITDQEMSLQLQVFLSEAFWIGL---RNNSGWRWEDGSPL 149
DB 79 QKTWNEHRLCASQKSSLLQQLQNTDELDFMS--SSQFYWIGLSYSEHTAWLWENGSA 136
QY 150 NFRSITSSNSF----VQTCGAINKNG-LQASSCEVPLHGVCCK 186
DB 137 --SQYLFPSFETFNKNCIAYNPNGNALDESCEDKNRYICKQ 176
RESULT 3
CD94_PANTR
ID_CD94_PANTR STANDARD; PRT; 179 AA.
AC Q9MZ41;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
lectin-like receptor subfamily D, member 1).
GN KLRD1 OR CD94.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]_TaxID=9598;
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20350666; PubMed=10994168;
RA Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,
RA Muir D.G., Canavez F., Cooper S.L., Valiante N.M., Lanier L.L.,
RA Parham P.;
RT "rapid evolution of NK cell receptor systems demonstrated by
comparison of chimpanzees and humans."
RL Immunity 12:687-698 (2000).
RN [2]
RP ALTERNATIVE SPLICING.
RX MEDLINE=21623889; PubMed=11751968;
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RA Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,
RA Cleland S., Guethlein L.A., Uhrberg M., Parham P.;
RT "Conservation and variation in human and common chimpanzee CD94 and
RT NK2 genes."
RL J. Immunol. 168:240-252 (2002).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
CC members.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment-Additional isoforms seem to exist;
CC Name=1; Synonyms=CD94-A;
CC IsoId=Q9MZ41-1; Sequences=Displayed;
CC Name=2; Synonyms=CD94-B;
CC IsoId=Q9MZ41-2; Sequences=VSP 003056;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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CC or send an email to license@isb-sib.ch).
DR EMBL; AF259054; AAF86964.1; -.
DR HSSP; P22897; 1EGG.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 89 174 BY SIMILARITY.
FT DISULFID 152 166 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 105 105 L -> LQ (in isoform 2).
FT VARSPLIC 105 105 /FTId=VSP 003056.
SQ SEQUENCE 179 AA; 20493 MW; 7244D99E8D9587E7 CRC64;
Query Match 19.0%; Score 194.5; DB 1; Length 179;
Best Local Similarity 32.7%; Pred. No. 1.3e-11;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;
QY 35 CSCLVAITLGLTAVLLSVLLYQWILCOGSN--YSTCASCPCSPDRMMKYGNHCYFVSVE 92
DB 20 CLSLMA-TLIGLLKNSFTKLSIEPAFTPGFNLELQKSDCCSCQKWKVGRNCYFISSE 78
QY 93 EKDWSSLEFFCLARDSHLIVITDQEMSLQLQVFLSEAFWIGL---RNNSGWRWEDGSPL 149
DB 79 QKTWNEHRLCASQKSSLLQQLQNTDELDFMS--SSQFYWIGLSYSEHTAWLWENGSA 136
QY 150 NFRSITSSNSF----VQTCGAINKNG-LQASSCEVPLHGVCCK 186
DB 137 --SQYLFPSFETFNKNCIAYNPNGNALDESCEDKNRYICKQ 176
RESULT 4
CLE2_HUMAN
ID_CLE2_HUMAN STANDARD; PRT; 149 AA.
AC Q92478; Q9UB84;
DT 28-FEB-2003 (Rel. 41, Created)
```

10-OCT-2003 (Rel. 42, Last sequence update)
 10-OCT-2003 (Rel. 42, Last annotation update)
 C-type lectin superfamily member 2 (Activation-induced C-type lectin).
 CLECSF2 OR AICL.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97190245; PubMed=9038101;
 RA Hamann J., Montgomery K.T., Lau S., Kucherlapati R., van Lier R.A.W.;
 RT "AICL, a new activation induced antigen encoded by the human NK gene
 complex.";
 RL Immunogenetics 45:295-300(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99173880; PubMed=10072769;
 RA Yokoyama-Kobayashi M., Yanaguchi T., Sekine S., Kato S.;
 RT "Selection of cDNAs encoding putative type II membrane proteins on the
 cell surface from a human full-length cDNA bank.";
 RL Gene 228:161-167(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RT TISSUE=Urinary bladder;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonfield G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
 CC -!- TISSUE SPECIFICITY: Expressed preferentially in lymphoid tissues,
 CC and in most hematopoietic cell types.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC
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 CC
 CC EMBL; X96719; CAA65480.1; -;
 CC EMBL; AB015628; BAA76495.1; -;
 CC EMBL; BC005254; AA05254.1; -;
 CC Genew; HGNC:2053; CLECSF2.
 CC MIM; 603242; -;
 CC GO; GO:0005887; C: integral to plasma membrane; TAS.
 CC GO; GO:0005930; F: lectin; TAS.
 CC GO; GO:0006960; P: antimicrobial humoral response (sensu Inver. . .); TAS.
 CC InterPro; IPR001304; Lectin_C.
 CC Pfam; PF00059; lectin_c; 1.
 CC SMART; SM00034; CLECT; 1.
 CC PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
 CC PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
 KW Glycoprotein; Transmembrane; Lectin; Signal-anchor.

FT DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 8 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 26 149 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 42 145 C-TYPE LECTIN.
 FT DISULFID 46 63 BY SIMILARITY.
 FT DISULFID 87 144 BY SIMILARITY.
 FT DISULFID 123 136 BY SIMILARITY.
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 79 79 M -> T (IN REF. 3).
 FT CONFLICT 107 107 D -> H (IN REF. 1).
 SQ SEQUENCE 149 AA; 17307 MW; 0B4FED23424F6C55 CRC64;
 Query Match 17.1%; Score 175; DB 1; Length 149;
 Best Local Similarity 32.2%; Pred. No. 8e-10;
 Matches 37; Conservative 24; Mismatches 48; Indels 6; Gaps 3;
 QY 75 CPDRWMKYGNHCYFVSVEEKDWSSLEFCLARDSHLLVITDQMSLLQVFLSEAFQWIG 134
 DB 35 CPYDWIGFQNKCYFSGEEDGWNSSKYNCTGADLTIIIDNIEEMNFRKYKCSDDHWIG 94
 QY 135 L--RNSGWRWEDGSPINFSRISNSFVOTCGAINKNGQASCEVPLHGVCCK 186
 DB 95 LKWKAKRTG-QWVDGA--TTFKSGMGSGCAYLSDGATARCYTERTKWKCRK 146
 RESULT 5
 V239 FOWPV STANDARD; PRT; 163 AA.
 ID V239 FOWPV STANDARD; PRT; 163 AA.
 AC P14371; Q9JS00;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative C-type lectin protein FPV239 (BamHI-ORF8).
 FN FPV239.
 OS Fowlpox virus (FPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Avipoxvirus.
 OC NCBI_TaxID=10261;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20193820; PubMed=10729156;
 RA Afonso C.L., Tulman E.R., Lu Z., Zaak L., Kutish G.F., Rock D.L.;
 RT "The genome of fowlpox virus.";
 RL J. Virol. 74:3815-3831(2000).
 RN [2]
 RP SEQUENCE OF 1-116 FROM N.A.
 RC STRAIN=PP-9 / Isolate HP-438;
 RX MEDLINE=88229622; PubMed=2836548;
 RA Tomley F., Binns M., Campbell J., Boursnell M.E.G.;
 RT "Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment
 RT of fowlpox virus.";
 RL J. Gen. Virol. 69:1025-1040(1988).
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC
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 CC
 CC EMBL; AF198100; AAF44583.1; -;
 CC EMBL; D00295; BAA00203.1; -;
 CC PIR; H29963; WWVZP8.
 CC HSP; P05140; 2AFP.
 CC InterPro; IPR001304; Lectin_C.
 CC Pfam; PF00059; lectin_c; 1.
 CC SMART; SM00034; CLECT; 1.
 CC PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.

[illegible]

DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 KW SIGNAL; LECTIN. 1. 26 BY SIMILARITY.
 FT CHAIN 27 175 PANCREATIC BETA CELL GROWTH FACTOR.
 FT DOMAIN 38 173 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 40 51 BY SIMILARITY.
 FT DISULFID 68 171 BY SIMILARITY.
 FT DISULFID 146 163 BY SIMILARITY.
 SQ SEQUENCE 175 AA; 19940 MW; 3854F36BA35D17CE CRC64;
 Query Match 14.4%; Score 147.5; DB 1; Length 175;
 Best Local Similarity 24.6%; Pred. No. 4.1e-07;
 Matches 42; Conservative 34; Mismatches 72; Indels 23; Gaps 7;
 QY 38 LVAITLGLTAVLLS-VLLY-QWILCOGSNYSTCASCPCSPDRWKKYGNHCYFVSVEKDW 96
 Db 2 MLPMLCRMWMLLSCLMFLSWGEGESQKLPSSRITCPGSGVAYGYCYSLILIPQTM 61
 QY 97 -NSSLEFCLARDSHLLVITDQEMSLLOVFLSEA-----FCWIGLR-----NNSGWR 142
 Db 62 SNAELSCQMHPFSGHLAFLLSTGEITFVSSLVKNLSLTAYQYIWIIGHDPHSGTLENGSGWK 121
 QY 143 WEDGSPNFSRISNSFVQT-----CGAIN-KNGLQA-----SCCEVPLHGVCV 185
 Db 122 WSSSNVLTFTYWNERNPSIAADRGYCAVLSQKSGFQKWRDFNCENELPYICK 172
 RESULT 8
 PAP3 MOUSE STANDARD; PRT; 174 AA.
 ID PAP3 MOUSE STANDARD; PRT; 174 AA.
 AC 009049;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Pancreaticis-associated protein 3 precursor (REG III-gamma).
 GN PAP3 OR REG3G.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver, and Pancreas;
 RX MEDLINE=97208868; PubMed=9055810;
 RA Narushima Y., Unno M., Nakagawara K.-I., Mori M., Miyashita H.,
 RA Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H.,
 RA Okamoto H.;
 RT "Structure, chromosomal localization and expression of mouse genes
 RT encoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma.";
 RL Gene 185:159-168(1997).
 CC -!- FUNCTION: Might be a stress protein involved in the control of
 CC bacterial proliferation.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Constitutively expressed in the small
 CC intestine, moderately in colon and at an extremely low level in
 CC healthy pancreas.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; D63361; BAA18930.1; -;
 DR EMBL; D63362; BAA18931.1; -;
 DR HSSP; P05451; 1LIT.
 DR MGD; MGI:109406; Reg3g.
 DR InterPro; IPR001304; Lectin C.
 DR InterPro; IPR003990; Pancreat_1.
 DR Pfam; PF00059; lectin_c; 1.

DR PRINTS; PR01504; PNCREATITSAP.
 DR SMART; SM00034; CLCCT; 1.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
 DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
 KW SIGNAL; LECTIN; Inflammatory response; Acute phase; Multigene family.
 FT CHAIN 1 26 PANCREATITIS-ASSOCIATED PROTEIN 3.
 FT DOMAIN 27 174 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 40 51 BY SIMILARITY.
 FT DISULFID 68 170 BY SIMILARITY.
 FT DISULFID 145 162 BY SIMILARITY.
 SQ SEQUENCE 174 AA; 19307 MW; 5575B9E56A4D8CEF CRC64;
 Query Match 14.4%; Score 147; DB 1; Length 174;
 Best Local Similarity 26.5%; Pred. No. 4.5e-07;
 Matches 45; Conservative 30; Mismatches 73; Indels 22; Gaps 7;
 QY 38 LVAITLGLTAVLLS-VLLY-QWILCOGSNYSTCASCPCSPDRWKKYGNHCYFVSVEKDW 96
 Db 2 LPTRITIMSWMLLSCLMFLSQVGEVAKKADAPSSRSSCPKGSRAVGYCYVALFSVSKNW 61
 QY 97 NSSLEFCLARDS-HLLVITDQEMSLLOVFL-----SEAFWIGLR-----NNSGWR 142
 Db 62 YDADMACQKRPSPGHLVSVLSGAEASFLSSMIKSGNSGQYVWIGLHDPPTLGYEPNRGWE 121
 QY 143 WEDGSPNFSRISNS--SFVQTGAINK-NGL--OASSCEVPLHGVCV 185
 Db 122 WSNADVWNYINWEINPSSSSNGHCGTLRSAGFLKWRNYCNLELPVCK 171
 RESULT 9
 CHBB CROHO STANDARD; PRT; 117 AA.
 ID CHBB CROHO STANDARD; PRT; 117 AA.
 AC P81503;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE CHB-B beta subunit.
 OS Crotales horridus horridus (Timber rattlesnake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scieroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Crotalus.
 OX NCBI_TaxID=8747;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=96420502; PubMed=8823201;
 RA Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M.,
 RA Smith A.I., Lopez J.A., Berndt M.C.;
 RT "Binding of a novel 50-kilodalton alboaggregin from Trimeresurus
 RT albolabris and related viper venom proteins to the platelet membrane
 RT glycoprotein Ib-IX-V complex. Effect on platelet aggregation and
 RT glycoprotein Ib-mediated platelet activation.";
 RL Biochemistry 35:12629-12639(1996).
 CC -!- FUNCTION: Binds to platelet GPIb/IX receptor system, inhibits VWF
 CC binding, and stimulates agglutination.
 CC -!- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 DR InterPro; IPR002353; AntifreezeII.
 DR InterPro; IPR001304; Lectin C.
 DR Pfam; PF00059; lectin_c; 1.
 DR PRINTS; PR00156; ANTIPEEEZEII.
 DR SMART; SM00034; CLCCT; 1.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
 DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
 KW LECTIN.
 FT DOMAIN 9 116 C-TYPE LECTIN.
 FT DISULFID 2 13 BY SIMILARITY.
 FT DISULFID 30 115 BY SIMILARITY.
 FT DISULFID 92 92 INTERCHAIN (WITH C-81 IN ALPHA CHAIN)
 FT DISULFID 95 107 (POTENTIAL).
 FT DISULFID 95 107 BY SIMILARITY.

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SQ SEQUENCE 117 AA; 13888 MW; 07835BBCB61E9EAD CRC64;
Query Match 14.3%; Score 146; DB 1; Length 117;
Best Local Similarity 28.4%; Pred. No. 3.6e-07;
Matches 33; Conservative 20; Mismatches 57; Indels 6; Gaps 3;
QY 75 CPDRWMKYGNHCYFVSVEEKDWNSSLEFCLARD--HLLVITDQMSLLQVLSFAFCW 132
Db 2 CFSQNSYEGHCYRVFQEQMTWDAKFCQQHTGHLVFSRSESEVDFVLSLKFDLFW 61
QY 133 IGLR---NNSGWRWEDGSPNFRISNSFVQTCGAINKGLQASCEVPLHGVCV 185
Db 62 MGRDITWNERRLQWSDTKVNYKAWSAEPICVCRATDNCWL-STSCSKTHNVVCK 116

RESULT 10
PAP1_MOUSE
ID PAP1_MOUSE STANDARD; PRT; 175 AA.
AC P35230;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pancreatitis-associated protein 1 precursor (REG III-beta).
GN PAP OR PAP1 OR REG3B.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=93176807; PubMed=7679928;
RA Itoh T., Teraoka H.;
RT "Cloning and tissue-specific expression of cDNAs for the human and
mouse homologues of rat pancreatitis-associated protein (PAP).";
RL Biochim. Biophys. Acta 1172:184-186(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=97208668; PubMed=9055810;
RA Narushima Y., Unno M., Nakagawara K.-I., Mori M., Miyashita H.,
RA Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H.,
RA Okamoto H.;
RT "Structure, chromosomal localization and expression of mouse genes
encoding type III Reg, RegII alpha, RegIII beta, RegIII gamma.";
RL Gene 185:159-168(1997).
CC -!- FUNCTION: Might be a stress protein involved in the control of
bacterial proliferation.
CC -!- SUBCELLULAR LOCATION: SECRETED. FOUND IN THE APICAL REGION OF
PANCREATIC ACINAR CELLS (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: Constitutively expressed in the small
intestine, moderately in colon and at an extremely low level in
healthy pancreas.
CC -!- INDUCTION: Appears in pancreatic juice after induction of
pancreatic inflammation.
CC -!- DISEASE: Overexpressed during the acute phase of pancreatitis.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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EMBL; D13509; BAA02727.1; -
DR EMBL; D63359; BAA18928.1; -
DR EMBL; D63360; BAA18929.1; -
DR FIR; S29822; S29822.
DR HSSP; P05451; ILIT.
DR MGD; MGI:97478; Pap.
InterPro; IPR001304; Lectin_C.

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DR InterPro; IPR003990; Pancreatis_ac.
DR Pfam; PF00059; lectin c; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Signal; Lectin; Inflammatory response; Acute phase; Multigene family.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 175 PANCREATITIS-ASSOCIATED PROTEIN 1.
FT DOMAIN 38 173 C-TYPE LECTIN (LONG FORM).
FT DISULFID 40 51 BY SIMILARITY.
FT DISULFID 68 171 BY SIMILARITY.
FT DISULFID 146 163 BY SIMILARITY.
SQ SEQUENCE 175 AA; 19476 MW; 44B3101171E79775 CRC64;

Query Match 13.4%; Score 137.5; DB 1; Length 175;
Best Local Similarity 25.7%; Pred. No. 3.7e-06;
Matches 46; Conservative 28; Mismatches 70; Indels 35; Gaps 9;
QY 33 PSCSLVAITLGLTAVLLSVLLYQWILCOGNSYTCASCP---SCPDRWMKYGNHCY 89
Db 3 PPTACSV-----MSWMLLSCLM--LLSQVQGEDSLKNIPSAISCPKGSQAYGSCYA 53
QY 89 FSVEEKDWNSSLEFCLAR--DSHLLVITDQMSLLQVFL-----SEAFWIGLR----- 136
Db 54 LFIQIPQTFDAELACQKPGHVLVNSAEASFSSVMYKRTGNSYQYTWIGLHDPVLGA 113
QY 137 --NNSGWRWEDGSPNFRISNSFVQT---CGAINK-NGL---QASCEVPLHGVCV 185
Db 114 EPNGGGSWNSNDVMYFNWERNPFTALDRAFGSLSRASGLKWDTCVFKLPVCK 172

RESULT 11
LITH RAT
ID LITH RAT STANDARD; PRT; 165 AA.
AC P10758;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lithostathine precursor (Pancreatic stone protein) (PSP) (Pancreatic
thread protein) (PTP) (Islet of langerhans regenerating protein) (REG)
DE (Islet cells regeneration factor) (ICRF).
GN REG1 OR REG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91093273; PubMed=1985964;
RA Rouquier S., Verdier J.M., Iovanna J., Dagorn J.-C., Giorgi D.;
RT "Rat pancreatic stone protein messenger RNA. Abundant expression in
mature exocrine cells, regulation by food content, and sequence
identity with the endocrine reg transcript.";
RL J. Biol. Chem. 266:786-791(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88115343; PubMed=2963000;
RA Terazono K., Yamamoto H., Takasawa S., Shiga K., Yonemura Y.,
RA Tochino Y., Okamoto H.;
RT "A novel gene activated in regenerating islets.";
RL J. Biol. Chem. 263:2111-2114(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93326645; PubMed=7916640;
RA Dusetti N.J., Frigerio J.M., Dagorn J.-C., Iovanna J.L.;
RT "Rapid PCR cloning and sequence determination of the rat
lithostathine gene.";
RL Biochim. Biophys. Acta 1174:99-102(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RA Miyashita H., Suzuki Y., Watanabe T., Unno M., Moriizumi S.,

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RA Yonekura H., Okamoto H.;
RT "Structure and characterization of rat Reg I gene.";
RL Seikagaku 65:1082-1082(1993).
RN [5]
RP SEQUENCE OF 22-69.
RC TISSUE=Pancreas;
RX MEDLINE=90031455; PubMed=2680252;
RA Adrich Z., de Caro A.M., Guidoni A.A., Woudstra M.E., Rovey M.;
RT "Characterization in rat pancreatic juice of a protein homologous to
RL the human pancreatic stone protein.";
RL Comp. Biochem. Physiol. 93B:793-797(1989).
CC -!- FUNCTION: Might act as an inhibitor of spontaneous calcium
CC carbonate precipitation.
CC -!- TISSUE SPECIFICITY: Expressed only in regenerating islets, but
CC not in normal pancreatic islets, insulinomas or regenerating
CC liver.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
DR EMBL; L07512; AAA41533.1; -
DR EMBL; M62930; AAA41974.1; -
DR EMBL; M18962; AAA42028.1; -
DR EMBL; D26164; BAA05149.1; -
DR PIR; A28351; A28351.
DR HSP; P05451; LLIT.
DR InterPro; IPR001304; Lectin C.
DR InterPro; IPR003990; Pancreatis_ac.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR CARBOHYD 129 129 N-LINKED (GLCNAC...) (POTENTIAL).
KM Glycoprotein; Signal; Lectin.
SQ SEQUENCE 165 AA; 18672 MW; 9861EB236B82CF8A CRC64;
-----
Query Match 13.4%; Score 137; DB 1; Length 165;
Best Local Similarity 27.2%; Pred. No. 3.8e-06;
Matches 43; Conservative 23; Mismatches 68; Indels 24; Gaps 7;
Qy 49 VLLSVLYQWLCOGSNYSTSCSPS-----CPDRMKYGNHCYFVSVEKDWNSSLEFCL 104
Dy 8 ILLSLCLM---VLSPSQGEAEEDLPASRITCPGSGNAYSSCYFYMEDHLSWAEADLFQC 64
Qy 105 ARDS-HLLVITDQMSLLQVFLSE-----AFQVIGL---PNSGWRWEDGSPLNF---- 151
Dy 65 NMNSGYLVLSVLSQAEGNFLASLIESGTTAAVWVIGLHDPKNNRRHWRHWSGSLFLYKSWD 124
Qy 152 SRISSNSFVQPCGAINKNG-----LQASSCEVPLHGVCX 185
Dy 125 TGYNNNSRGYCVSVTSNSGYKKWRDNSCDQLGFSVCK 162
-----
RESULT 12
AMP HEMAM STANDARD; PRT; 163 AA.
AC P05140;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

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DE Antifreeze protein precursor (AFP).
OS Hemipterus americanus (Sea raven).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottoidei; Hemipteridae; Hemipteridae; Hemipteridae; Hemipteridae;
RN NCBI_TaxID=8094;
RX SEQUENCE FROM N.A.
MEDLINE=87057207; PubMed=3782083;
RA NG N.F.L., Trinn K.-Y., Hew C.-L.;
RT "Structure of an antifreeze polypeptide precursor from the sea raven,
RT Hemipterus americanus.";
RL J. Biol. Chem. 261:15690-15695(1986).
RN [2]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
MEDLINE=90036986; PubMed=2572595;
RA Hayes P., Scott G.K., Ng N.F.L., Hew C.-L., Davies P.L.;
RT "Cystine-rich type II antifreeze protein precursor is initiated from
RT the third AUG codon of its mRNA.";
RL J. Biol. Chem. 264:18761-18767(1989).
RN [3]
RP DISULFIDE BONDS, AND SIMILARITY TO C-TYPE LECTINS.
MEDLINE=92355557; PubMed=1644794;
RA NG N.F.L., Hew C.-L.;
RT "Structure of an antifreeze polypeptide from the sea raven. Disulfide
RT bonds and similarity to lectin-binding proteins.";
RL J. Biol. Chem. 267:16069-16075(1992).
RN [4]
RP STRUCTURE BY NMR, AND REVISIONS TO DISULFIDE BONDS.
MEDLINE=98206886; PubMed=9537986;
RA Gronwald W., Loewen M.C., Lix B., Daugulis A.J., Soemichsen F.D.,
RA Davies P.L., Sykes B.D.;
RT "The solution structure of type II antifreeze protein reveals a new
RT member of the lectin family.";
RL Biochemistry 37:4712-4721(1998).
CC -!- FUNCTION: Antifreeze proteins lower the blood freezing point.
CC -!- SIMILARITY: BELONGS TO THE TYPE-II AFP FAMILY. TYPE 2 AFP ARE
CC CYSTINE-RICH.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
DR EMBL; J02593; AAA49617.1; ALT_INIT.
DR EMBL; J05100; AAA49618.1; -
DR PIR; A34313; A34313.
DR PDB; 2AFP; 23-DEC-98.
DR InterPro; IPR002353; Antifreeze2.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR Antifreeze protein; Lectin; Signal; 3D-structure.
FT SIGNAL 1 17 POTENTIAL.
FT PROPEP 18 34
FT CHAIN 35 163 ANTIFREEZE PROTEIN.
FT DOMAIN 39 163 C-TYPE LECTIN (LONG FORM).
FT DISULFID 41 52
FT DISULFID 69 159
FT DISULFID 103 134
FT DISULFID 123 145
FT DISULFID 135 151
FT CONFLICT 38 38 P -> G (IN REF. 2).
FT STRAND 52 53
FT HELIX 62 72

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FT STRAND 75 76
FT HELIX 83 91
FT STRAND 96 96
FT STRAND 101 101
FT STRAND 110 110
FT TURN 131 132
FT STRAND 135 135
FT STRAND 138 138
FT STRAND 146 146
FT STRAND 149 149
FT STRAND 159 161
SQ SEQUENCE 163 AA; 17509 MW; 52C2D2B4F65E8A47 CRC64;

Query Match
Best Local Similarity 13.3%; Score 136; DB 1; Length 163;
Matches 26; Conservative 10; Mismatches 42; Indels 4; Gaps 2;

QY 73 PSCPDRWMKYGNHCYFVSVEEKDWNLSLEFCLARDSHLLVITDQMSLILQVFLSEAFQW 132
Db 39 PNCPCAGWQPLGDCRIYETAMTWALAEATNCMLGGLASIHQSQEHSPLOT-LNAGVW 97

QY 133 IG---LRNNSGWRWEGDGLP 151
Db 98 IGGSAQLQAGAWTSDGTPMNF 119

RESULT 13
LITH_BOVIN STANDARD; PRT; 175 AA.
AC P23132;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lithostathine precursor (pancreatic stone protein) (PSP) (Pancreatic
DE thread protein) (PTP) (Islet of Langerhans regenerating protein) (REG)
DE (Islet cells regeneration factor) (ICRF).
GN PTP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90368981; PubMed=2394826;
RA de la Monte S.M., Ozturk M., Wands J.R.;
RT "Enhanced expression of an exocrine pancreatic protein in Alzheimer's
RL disease and the developing human brain.";
RL J. Clin. Invest. 86:1004-1013(1990).
RN [2]
RP SEQUENCE OF 38-138 AND 141-175.
RX MEDLINE=91197388; PubMed=2085387;
RA Cai L., Harris W.R., Marshak D.R., Gross J., Crabb J.W.;
RT "Structural analysis of bovine pancreatic thread protein.";
RL J. Protein Chem. 9:623-632(1990).
RN [3]
RP SEQUENCE OF 38-85 AND 141-175.
RX MEDLINE=85298214; PubMed=3862086;
RA Gross J., Brauer A.W., Bringham R.F., Corbett C., Margolies M.N.;
RT "An unusual bovine pancreatic protein exhibiting pH-dependent
RT globule-fibril transformation and unique amino acid sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:5627-5631(1985).
CC -1- FUNCTION: Might act as an inhibitor of spontaneous calcium
CC carbonate precipitation.
CC -1- SUBUNIT: Cleaved to give an A chain and a B chain joined by a
CC disulfide bond.
CC -1- TISSUE SPECIFICITY: In pancreatic acinar cells.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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CC
CC -----
DR EMBL; M59794; AAA30750.1; -.
DR PIR; A37194; A37194.
DR HSSP; P05451; LODD.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatins.ac.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Glycoprotein; Signal; Lectin.
FT SIGNAL 1 26
FT PROPEP 27 37
FT CHAIN 38 175
FT CHAIN 38 138
FT CHAIN 141 175
FT DOMAIN 38 173
FT DISULFID 40 51
FT DISULFID 68 171
FT DISULFID 146 163
FT CONFLICT 84 85
FT SEQUENCE 175 AA; 19334 MW; C270EE70B7E91D6A CRC64;

Query Match
Best Local Similarity 13.1%; Score 134.5; DB 1; Length 175;
Matches 48; Conservative 27; Mismatches 63; Indels 37; Gaps 9;

QY 42 TLGL--LTAVLTLVLLYQWILCOGSNYSCASCP-----SCPDRWMKYGNHCYFVSVEEKD 95
Db 4 SLGLPRLSWMLLSCLM---LLSQIOGNSQKELPSARISCPGSGSMAYRSHCYALFKTPKT 60

QY 96 WNSLLEFCLARD--HLLVITDQMSLILQVFL-----SEAFQWIGLR-----NNSGW 141
Db 61 WMDADIACOKRPSGHLVSLGAESEFVASLVRRNNLTQSDIWLGHDPTEGSEANAGW 120

QY 142 RWEDGSPLNF-----SRISNSFVQTCGAINKNG---LQASCEVPLHGVC 185
Db 121 EWISNDVLNVAVWETDPAALISPGY---CGSLSRSSGYLKWDRHNCNLNLPYVCK 172

RESULT 14
PAP2_MOUSE STANDARD; PRT; 175 AA.
AC O09037;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pancreatitis-associated protein 2 precursor (Lithostathine 3) (Islet
DE of Langerhans regenerating protein 3) (REG 3) (REG III-alpha).
GN PAP2 OR REG3A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Liver, and Pancreas;
RX MEDLINE=97208868; PubMed=9055810;
RA Narushima Y., Unno M., Nakagawara K.-I., Mori M., Miyashita H.,
RA Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H.,
RA Okamoto H.;
RT "Structure, chromosomal localization and expression of mouse genes
RT encoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma.";
RL Gene 185:159-168(1997).
CC -1- FUNCTION: Might be a stress protein involved in the control of
CC bacterial proliferation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Small intestine and pancreas.
CC -1- DISEASE: Overexpressed during the acute phase of pancreatitis.

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CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
CC EMBL; D63356; BAA18925.1; -.
CC EMBL; D63357; BAA18926.1; -.
CC EMBL; D63358; BAA18927.1; -.
CC HSP; P05451; ILIT.
CC MCD; MGI:109408; Reg3a.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR003990; Pancreatins_ac.
CC Pfam; PF00059; lectin_c; 1.
CC PRINTS; PR01504; PNCREATITISAP.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C-TYPE LECTIN_1; 1.
CC PROSITE; PS00041; C-TYPE LECTIN_2; 1.
CC Signal; Lectin; Inflammatory response; Acute phase; Multigene family.
CC SIGNAL 1 26
CC CHAIN 27 175 PANCREATITIS-ASSOCIATED PROTEIN 2.
CC DOMAIN 38 173 C-TYPE LECTIN (LONG FORM).
CC DISULFID 40 51 BY SIMILARITY.
CC DISULFID 68 171 BY SIMILARITY.
CC DISULFID 146 163 BY SIMILARITY.
CC SEQUENCE 175 AA; 19539 MW; 3E311B3976E80F11 CRC64;
Query Match 13.1%; Score 134.5; DB 1; Length 175;
Best Local Similarity 28.2%; Pred. No. 7.1e-06;
Matches 49; Conservative 21; Mismatches 69; Indels 35; Gaps 8;
Qy 41 ITLGLLFAVLVLLVLYQWILCOGNSYTCASCP--SCPDRMKYGNHCYFSVEEKOWNS 98
Db 5 LVLSISWMLLSCLLFVQV-QGEDFQKEVPSPTSCPMGYKAYRSHCYALVMTPKSWFQ 63
Qy 99 SLEFLARDS-HLIVTDNQMSLLQVFLSAF-----CWIGLR-----NNSGRWE 144
Db 64 ADLVCKRRPSGHLVLSGGASVSVSLVNGRVNVDYQDIWTLGHDPTMGQPPNGGGWEWS 123
Qy 145 DGSPLNF-----SRISNSSFVOTCGAINKNGLOQSS-----CEVPLHGVC 185
Db 124 NSDVLYNLWDDPSSTVNRGCGS-----LTASSGFLKWDYCYDGTLPVCK 172
RESULT 15
MMHB AGKHA STANDARD; PRT; 146 AA.
AC Q9YI92;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mamushigin beta chain precursor.
OS Agkistrodon halys blomhoffii (Mamushi) (Gloydius blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Viperidae; Crotalinae; Gloydius.
OC NCBI_TaxID=242054;
RN [1]
RP SEQUENCE FROM N.A.; SEQUENCE OF 24-56, SUBUNIT, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=98319530; PubMed=9657448;
RA Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasaki T., Handa M.,
RA Suzuki M., Matsui T., Titani K., Yoshioka A.;
RT "The cDNA cloning and molecular characterization of a snake venom
RT platelet glycoprotein Ib-binding protein, mamushigin, from Agkistrodon
RT halys blomhoffii venom.";
RL Thromb. Haemost. 79:1199-1207(1998).
CC -!- FUNCTION: Binds to platelet glycoprotein Ib and enhances platelet
CC aggregation at low-shear stress. At high-shear stress, aggregation

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CC is inhibited.
CC -!- SUBUNIT: Heterodimer of alpha and beta chains; disulfide-
CC linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=15413; MW_ERR=6; METHOD=Electrospray;
CC RANGE=24-146.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
CC EMBL; AB019616; BAA34425.1; -.
CC HSP; P23807; LIXX.
CC GO; GO:0005576; C:extracellular; IC.
CC GO; GO:0007596; P:blood coagulation; IDA.
CC InterPro; IPR001304; Lectin_C.
CC Pfam; PF00059; lectin_c; 1.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C-TYPE LECTIN_1; 1.
CC PROSITE; PS00041; C-TYPE LECTIN_2; 1.
CC Blood coagulation; Lectin; Signal.
CC SIGNAL 1 23
CC CHAIN 24 146 MAMUSHIGIN BETA CHAIN.
CC DOMAIN 32 143 C-TYPE LECTIN.
CC DISULFID 25 36 BY SIMILARITY.
CC DISULFID 53 142 BY SIMILARITY.
CC DISULFID 98 98 INTERCHAIN (WITH C-103 IN ALPHA CHAIN)
CC (BY SIMILARITY).
CC DISULFID 119 134 BY SIMILARITY.
CC SEQUENCE 146 AA; 17064 MW; 9EDA84BDCC24E76D CRC64;
Query Match 13.1%; Score 134; DB 1; Length 146;
Best Local Similarity 28.6%; Pred. No. 6.5e-06;
Matches 36; Conservative 18; Mismatches 50; Indels 22; Gaps 6;
Qy 75 CPDRMKYGNHCYFSVEEKOWNSLEFCL--ARDSHLVITDNGE---MSLLQVFLSE 128
Db 25 CPDWSSEYEGHCYRVFQKEMTWEDAEKFCQQRKESHLVSFHSSEYDFVVSMTWPIIKY 84
Qy 129 AFCWIGLRNKGW-----RWEDGSPFNFSRISNSSFVOTCGAI---NKNGLOQSSCEVP 179
Db 85 DFWWIGL--NNIWNCEWVETDG-----TRLSHNAWITESECIAAKTTDNLWLRPCRT 137
Qy 180 LHGVCK 185
Db 138 YNVVCK 143
Search completed: August 10, 2004, 16:34:04
Job time : 14 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:29:18 ; Search time 37 Seconds

(without alignments)
1611.701 Million cell updates/sec

Title: US-09-811-367B-1

Perfect score: 1023

Sequence: 1 MTDSVIYSMLELTATQAQN.....GLQASSCEVLHGVCCKVRL 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 398377

Minimum DB seq length: 0

Maximum DB seq length: 189

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriaph.*
17: sp_bacteriaph.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1023	100.0	189	4	O43198
2	1007	98.4	189	4	O75613
3	548.5	53.6	188	11	O88713
4	525.5	51.4	188	11	Q64335
5	225	22.0	181	4	Q9NZS1
6	194.5	19.0	178	11	Q91ZW9
7	189.5	18.5	179	6	Q8MJ13
8	189.5	18.5	179	6	Q8MEY8
9	187	18.3	179	11	O35778
10	186.5	18.2	179	6	Q8MEY9
11	186.5	18.2	179	6	Q8MJ14
12	185	18.1	132	11	Q834K5
13	185	18.1	133	6	Q9GK90
14	184.5	18.0	159	6	Q8SPX0
15	184	18.0	183	13	Q802S7
16	183.5	17.9	179	11	O54708

17	183.5	17.9	179	11	O54707
18	180.5	17.6	158	11	Q80Z35
19	175.5	17.2	168	11	Q9JKF2
20	175.5	17.2	183	6	Q95J54
21	174.5	17.1	161	6	Q95JG4
22	173	16.9	175	11	Q9JKF3
23	167.5	16.4	185	6	Q9MZJ6
24	163.5	16.0	80	6	Q95UG6
25	163.5	16.0	80	6	Q95JG5
26	162.5	15.9	164	11	Q9EP94
27	162	15.8	156	11	Q7TSP6
28	161.5	15.8	162	6	Q8MJH4
29	161.5	15.8	162	6	Q8MJH3
30	161.5	15.8	173	4	Q9HD37
31	160.5	15.7	162	6	Q8MHY4
32	160	15.6	146	13	Q7T045
33	159.5	15.6	165	6	Q9GLF4
34	159	15.5	188	4	Q9NY25
35	157	15.3	137	4	Q8I2E9
36	156	15.2	154	4	Q8WUF7
37	155.5	15.2	142	11	Q8V119
38	155.5	15.2	142	11	Q8BHK7
39	155.5	15.2	187	4	Q9UKQ0
40	154	15.1	182	11	Q61972
41	153.5	15.0	142	11	Q8CJ86
42	152.5	14.9	185	6	Q9GLF3
43	150	14.7	168	4	Q96PA7
44	147	14.4	134	5	Q9XYX3
45	147	14.4	176	11	Q9D8Q7

ALIGNMENTS

RESULT 1

O43198 PRELIMINARY; PRT; 189 AA.
AC O43198
DT 01-JUN-1998 (TREMREL. 06, Created)
DT 01-JUN-1998 (TREMREL. 06, Last sequence update)
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
DE Mast cell function-associated antigen.
GN MAFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=98438735; PubMed=9765598;
RA Lamers M.B., Lamont A.G., Williams D.H.;
RT "Human MAFA has alternatively spliced variants.";
RL Biochim. Biophys. Acta 1399:209-212(1998).
DR EMBL: AF034952; AAC34731.1;
DR GO: GO:0016021; C:integral to membrane; TAS.
DR GO: GO:0003793; F:defense/immunity protein activity; TAS.
DR GO: GO:0005530; F:lectin; TAS.
DR GO: GO:0004872; F:receptor activity; TAS.
DR GO: GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR GO: GO:0006968; P:cellular defense response; TAS.
DR GO: GO:0006954; P:inflammatory response; TAS.
DR InterPro: IPR001304; lectin_c; 1.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT. 1.
DR PROSITE: PS50041; C TYPE LECTIN 2; 1.
SQ SEQUENCE 189 AA; 21073 MW; 15E042AD40B2B4F6 CRC64;

Query Match 100.0%; Score 1023; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 7.4e-105;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDSVIYSMLELTATQAQNDYGPQKSSSRKPSCLVAITLGLTAVLLSVLLQWIL 60

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Db 1 MTDSVIYMLPLPTAQNDYGPQKSSSSKPCSCLVATILGLTAVLLSVLLYQWIL 60
QY 61 CQGSNYSTCASCPCPDPRMKGNYHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
Db 61 CQGSNYSTCASCPCPDPRMKGNYHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
QY 121 LLOVFLSEAFQWIGLRNNSGWRWEDGSPINFSRISNSSNFVQTCGAINKNGLOASSCEVPL 180
Db 121 LLOVFLSEAFQWIGLRNNSGWRWEDGSPINFSRISNSSNFVQTCGAINKNGLOASSCEVPL 180
QY 181 HGVCCKVRL 189
Db 181 HGVCCKVRL 189

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RESULT 2

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O75613 PRELIMINARY; PRT; 189 AA.
AC O75613;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ITIM-containing receptor MAFA-L.
GN MAFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Butcher S., Arney K.L., Cook G.P.;
RT "MAFA-L, an ITIM-containing receptor encoded by the human NK cell gene
RT complex and expressed by basophils and NK cells.";
RL Eur. J. Immunol. 28:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99077194; PubMed=9862378;
RA Hanke T., Corral L., Vance R.E., Raullet D.H.;
RT "2F1 antigen, the mouse homolog of the rat 's1', is a lectin-like type
RT II transmembrane receptor expressed by natural killer cells.";
RL Eur. J. Immunol. 28:4409-4417(1998).
DR EMBL; AF081675; AAC32200.1; -.
DR EMBL; AF097358; AAD03719.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; LECTIN_C.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 189 AA; 21206 MW; FA9023F1523656A8 CRC64;

```

Query Match 98.4%; Score 1007; DB 4; Length 189;
 Best Local Similarity 98.4%; Pred. No. 4.3e-103;
 Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 MTDSVIYMLPLPTAQNDYGPQKSSSSKPCSCLVATILGLTAVLLSVLLYQWIL 60
Db 1 MTDSVIYMLPLPTAQNDYGPQKSSSSKPCSCLVATILGLTAVLLSVLLYQWIL 60
QY 61 CQGSNYSTCASCPCPDPRMKGNYHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
Db 61 CQGSNYSTCASCPCPDPRMKGNYHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
QY 121 LLOVFLSEAFQWIGLRNNSGWRWEDGSPINFSRISNSSNFVQTCGAINKNGLOASSCEVPL 180
Db 121 LLOVFLSEAFQWIGLRNNSGWRWEDGSPINFSRISNSSNFVQTCGAINKNGLOASSCEVPL 180
QY 181 HGVCCKVRL 189
Db 181 HWVCCKVRL 189

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RESULT 3

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O88713 PRELIMINARY; PRT; 188 AA.
AC O88713;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-
DE like receptor G1).
GN KLRG1 OR MAFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C.B-17 SCID;
RX MEDLINE=99077194; PubMed=9862378;
RA Hanke T., Corral L., Vance R.E., Raullet D.H.;
RT "2F1 antigen, the mouse homolog of the rat 's1', is a lectin-like type
RT II transmembrane receptor expressed by natural killer cells.";
RL Eur. J. Immunol. 28:4409-4417(1998).
RN [2]
RP SEQUENCE OF 2-188 FROM N.A.
RA Blaser C.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvevTACFeR; TISSUE=Spleen;
RX MEDLINE=21115136; PubMed=11220622;
RA Voehringer D., Kaufmann M., Pircher H.;
RT "Genomic structure, alternative splicing, and physical mapping of the
RT killer cell lectin-like receptor G1 gene (KLRG1), the mouse homologue
RT of MAFA.";
RL Immunogenetics 52:206-211(2001).
DR EMBL; AF097357; AAD03718.1; -.
DR EMBL; AJ010751; CAA09342.1; -.
DR EMBL; AF317727; AAK40082.1; -.
DR MGD; MGI:1355294; KLRG1.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR LECTIN; Receptor.
SQ SEQUENCE 188 AA; 21396 MW; 876336802EAL34F1 CRC64;

```

Query Match 53.6%; Score 548.5; DB 11; Length 188;
 Best Local Similarity 55.6%; Pred. No. 2.1e-52;
 Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

```

QY 1 MTDSVIYMLPLPTAQNDYGPQKSSSSKPCSCLVATILGLTAVLLSVLLYQWIL 60
Db 1 MADSSIVTLELPEAPQVQDESRLKAVLRPHLSRFAMVALGLLTIVILSLMYQRIL 60
QY 61 CQGSNYSTCASCPCPDPRMKGNYHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
Db 61 CQGSNYSTCASCPCPDPRMKGNYHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
QY 121 LLOVFLSEAFQWIGLRNNSGWRWEDGSPINFSRISNSSNFVQTCGAINKNGLOASSCEVPL 180
Db 121 LQVFLSEAFQWIGLRNNSGWRWEDGSPINFSRISNSSNFVQTCGAINKNGLOASSCEVPL 180
QY 181 HGVCCKV 187
Db 180 QWICKV 186

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RESULT 4

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Q64335 PRELIMINARY; PRT; 188 AA.
ID Q64335
AC Q64335;

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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MAFA protein.
DE MAFA.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=Testis;
RA Bocek Jr P., Gutmann M.D., Pecht I.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96016176; PubMed=7568140;
RA Gutmann M.D., Tal M., Pecht I.;
RT "A secretion inhibitory signal transduction molecule on mast cells is
  another C-type lectin.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).
DR EMBL; X97191; CAA65829.1; -.
DR EMBL; X97192; CAA65829.1; JOINED.
DR EMBL; X97193; CAA65829.1; JOINED.
DR EMBL; X97194; CAA65829.1; JOINED.
DR EMBL; X97195; CAA65829.1; JOINED.
DR EMBL; X97812; CAA56208.1; -.
DR PIR; I59421; I59421.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 188 AA; 21356 MW; 2CC8032D4D020B15 CRC64;

Query Match 51.4%; Score 525.5; DB 11; Length 188;
Best Local Similarity 53.5%; Pred. No. 7.2e-50;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MTDVSYLMELPTAQNDYGFQKSSKSPSCSLVAITLGLTAVLLSVLLYQWIL 60
DB 1 MADNSYSTLELPAPRPVQDSSRWKAVLHRCVSVLVMVALGLLTIVLMSLLYQRTL 60
QY 61 CGSNYSTCASCPCDRMKYGNHCYFVVEKDNSSLEFCLARDSHLLVITDQEMS 120
DB 61 CGSGKGFMCQRCRCPNLNWRNGSHCYFYSMERKDNSSLKFCADRGSHLLTTPDQGVN 120
QY 121 LLQVFLSEAFPCWTGLRNNSGWRWEDGSPNFSISSNFVQTCGAINKNGLOASSCEVPL 180
DB 121 LFQEVYGEDFYWLGRLDIDGWRWEDGFALSLS-ILNSVVKCGTTHRCGLHASSCEVAL 179
QY 181 HGVCKKV 187
DB 180 QWICEKV 186

RESULT 5
Q9NZS1 PRELIMINARY; PRT; 181 AA.
AC Q9NZS1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lectin-like receptor Fl, splice variant 1 KLRP1-si.
GN KLRP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20135860; PubMed=10671213;
RA Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,

Fernandez-Ruiz E.;
"Human KLRP1, a novel member of the killer cell lectin-like receptor
gene family: molecular characterization, genomic structure, physical
mapping to the NK gene complex and expression analysis.";
RL Eur. J. Immunol. 30:568-576(2000).
DR EMBL; AF175207; AAF37805.1; -.
DR GO; GO:0016020; C:membrane; TAS.
DR GO; GO:0030106; F:MHC class I receptor activity; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 181 AA; 21204 MW; 64642240CAE1B551 CRC64;

Query Match 22.0%; Score 225; DB 4; Length 181;
Best Local Similarity 33.6%; Pred. No. 1.1e-16;
Matches 51; Conservative 26; Mismatches 45; Indels 30; Gaps 6;

QY 44 GLTAVLLSVLLYQWILCOGSNYSTCASCPCDRMKYGNHCYFVVEKDNSSLEFC 103
DB 49 GLTTLTSLILL--VLQ-----SEWLKYGKCYFNSNEMKWSDSYVYC 92
QY 104 LARDSHLLVITDQEMSLQVFLSBA-FCWIGLRNNS---GWRWEDGSPNFSRISNSF 159
DB 93 LERKSHLLIHDQLEWAFIQKRLQNLNYVWIGLFTSLKMTWTWVDGSPID----SKIFF 148
QY 160 VQ-----TCGAINKNGLOASSCEVPLHGVCX 185
DB 149 IKGPAKENSAAIKSKIFSETCSSVFKWICQ 180

RESULT 6
Q91ZW9 PRELIMINARY; PRT; 178 AA.
AC Q91ZW9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SIGNR2.
GN CD209C OR SIGNR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX PubMed=11581173;
RA Park C.G., Takahara K., Umemoto E., Yashima Y., Matsubara K.,
RA Matsuda Y., Clausen B.E., Inaba K., Steinman R.M.;
RT "Five mouse homologues of the human dendritic cell C-type lectin, DC-
  SIGN. ";
RL Int. Immunol. 13:1283-1290(2001).
DR EMBL; AF373410; AAL13236.1; -.
DR MGD; MGI:2157945; Cd209c.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 178 AA; 21245 MW; 034F94CE02BD9032 CRC64;

Query Match 19.0%; Score 194.5; DB 11; Length 178;
Best Local Similarity 31.0%; Pred. No. 2.6e-13;
Matches 39; Conservative 23; Mismatches 53; Indels 11; Gaps 3;

QY 72 CPSCPDPMKYNHCYFVVEKDNSSLEFCLARDSHLLVITDQEMSLQVFLSE-AP 130
DB 45 CRPCPDWTVFQGCYFFSKFQGNWDSYNACRKLDAQLVVKSDDEQSFQOTSKEGY 104

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QY	131	CMWIG---LRNNSGHWEDGSPINFSRIS-----SNFSVQTCGAINKNGLOASCEVPL	180
Db	105	AWMLGSLDKHGRHWVDGSHLLFSFMKYWNKGFENNEEDCABFRGDGWDNAPCTIKK	164
QY	181	HGVCKK 186	
Db	165	YWICKK 170	
RESULT 7			
Q8MJ13			
ID	Q8MJ13	PRELIMINARY; PRT; 179 AA.	
AC	Q8MJ13;		
DT	01-OCT-2002 (TReMBLrel. 22, Created)		
DT	01-OCT-2002 (TReMBLrel. 22, Last sequence update)		
DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)		
DE	Natural killer cell receptor.		
GN	POPY-CD94.		
OS	Pongo pygmaeus (Orangutan).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.		
OX	NCBI_TaxID=9600;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22072192; PubMed=12077248;		
RA	Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;		
RT	"NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal		
RT	Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors		
RT	with MHC-C.;"		
RL	J. Immunol. 169:220-229 (2002).		
DR	EMBL; AF470384; AAM78484.1; -.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	GO; GO:0005529; F:sugar binding; IEA.		
DR	InterPro; IPR006209; EGF like.		
DR	InterPro; IPR001304; Lectin_C.		
DR	Pfam; PF00059; lectin_c; 1.		
DR	SMART; SM00034; CLECT; 1.		
DR	PROSITE; PS00041; C TYPE LECTIN_2; 1.		
DR	PROSITE; PS00022; EGF_1; 1.		
KW	Receptor.		
SQ	SEQUENCE 179 AA; 20566 MW; 6752CB8F0F9A2609 CRC64;		
Query Match 18.5%; Score 189.5; DB 6; Length 179;			
Best Local Similarity 28.6%; Pred. NO. 9.4e-13;			
Matches 50; Conservative 29; Mismatches 61; Indels 35; Gaps 7			
QY	38	LVATTLGLTAVLLSVLLYQWLCOGS-----NYSTCASCSPCDRWK	81
Db	11	LISLTGLICLSLMTATL---GILKNSTKLSIEPAFTPGDIDELQKDDCCSCOEKWWG	67
QY	82	YGNHCYFSEVEKDWNSSLEFLARDSHLLVITDNQEMSLQLVFLSEAFCWIGL---RNN	138
Db	68	YRCNCYFISSEQKTWNESRHLCAQSKSSLQLQNTDELDWS--SSQFYWIGLSVSEH	125
QY	139	SGHWEDGSPIN-----FSRISNSFVQTCGAINKNG-LOASCEVPLHGVCKK	186
Db	126	TAMLWENGSSLSQYLFPLFTFNP----KNCIAYNPNGNALDESCEDNRYICKQ	176
RESULT 8			
Q8MHY8			
ID	Q8MHY8	PRELIMINARY; PRT; 179 AA.	
AC	Q8MHY8;		
DT	01-OCT-2002 (TReMBLrel. 22, Created)		
DT	01-OCT-2002 (TReMBLrel. 22, Last sequence update)		
DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)		
DE	Natural killer cell receptor.		
GN	POPY-CD94.		
OS	Pongo pygmaeus (Orangutan).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.		
OX	NCBI_TaxID=9600;		


```

RT RT "Molecular cloning, expression pattern, and chromosomal mapping of pig
RT CD69."
RT RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF484234; AAL91547.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR SEQUENCE 159 AA; 18056 MW; 19373 BAE; 92AA69 CRC64;

Query Match 18.0%; Score 184.5; DB 6; Length 159;
Best Local Similarity 32.2%; Pred.No. 2.9e-12;
Matches 38; Conservative 19; Mismatches 52; Indels 9; Gaps 4;

QY 74 SCPRWKNYGNHCYYSVEKDWNSLEPCLARDSHLLVITNOE-MSLLQVFLSEAFQW 132
Db 43 SCPPDDTGYQTKYCFISKTKNTWTLAQSFCSCHHGATLALLESKEDMVFLLKHVGRAEHW 102
QY 133 IGLRNNSG--WRWEDGSPLN--FSRISSSFVQTGAINKNGLQASSCEVPLHGCKK 186
Db 103 IGLKNEGGQTKWNSGKEFNWFKLTGS----KNCFFLNSTEVGSMECEKNLHWICK 156

RESULT 15
Q802S7 PRELIMINARY; PRT; 183 AA.
AC Q802S7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C-type lectin.
GN Y-LEC1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NC NCBI_TaxID=9031;
PN [1]

```

RP SEQUENCE FROM N.A.
RA Rogers S., Shaw I., Ross N., Nair V., Rothwell L., Kaufman J.,
RA Kaiser P.;
RT "Analysis of part of the chicken Rfp-Y region reveals two novel lectin
RT genes, the first complete genomic sequence of a class I alpha-chain
RT gene, a truncated class II beta-chain gene, and a large CRI repeat.";
RL Submitted (JAN-2003) to the EMBL/Genbank/DBEB databases.
DR EMBL: AJ277927; CAD61337.1; -;
DR GO: GO:0005529; F:sugar binding; IEA.
DR GO: GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro: IPR002353; AntifreezeZell.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; lectin C; 1.
DR PRINTS: PR00356; ANTI-FREEZEII.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00411; C-type lectin 2; 1

```

SQ      SEQUENCE      183 AA;  20011 MW;  725DB7845867D341 CRC64;

Query Match      18.0%;  Score 184;  DB 13;  Length 183;
Best Local Similarity 29.3%;  Pred. NO. 3.9e-12;
Matches 51;  Conservative 20;  Mismatches 57;  Indels 46;  Gaps 6;

QY      22  YGPOQKSSSKSPSCSLVAITLGLLTAVLLSVLLYQWILCOGSNYSTCASCPCSPDRMK 81
       :  ::  ::  :  ||  ||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      33  HGTGRRSRVQIIAACALGTLSLVLVISTDFAH-----ACPNWVG 75

QY      82  YGNHCYFYSVEEKDNSSLEFCLARDLSLLVITONQMSLLQVFLSEAFQWIGL---RNN 138
       :  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  :
Db      76  FQCKYIYSKEENDWNSGREHNAHGAATIGSAEEMDFMRFPQGPANCVIGLHWEED 135

QY      139  SQWRWED-----GSPINFSRISNSNFVOTCGA-----INKNGLQASCEV 178
       :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      136  AITWVNCVITATNNWESGSP-----SPGCIHNAHFGGLITATV 177

```

Search completed: August 10, 2004, 16:34:58
Job time : 43 secs

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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:19:43 ; Search time 53 Seconds
(without alignments)
1007.575 Million cell updates/sec

Title: US-09-811-367B-1

Perfect score: 1023

Sequence: 1 WTDSVIYSMLELPTATQAGN.....GLQASCEVPLHGVCCKVRL 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1084940

Minimum DB seq length: 0
Maximum DB seq length: 189

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A Geneseq 25Jan04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1023	100.0	189	2	AAW88265 Human mas
2	1023	100.0	189	4	AAE11759 Human mas
3	1007	98.4	189	7	ADD25635 Binding d
4	548.5	53.6	188	4	AAE11760 Mouse mas
5	525.5	51.4	188	2	AAE11760 Mammalian
6	525.5	51.4	188	2	AAW88277 Rat mast
7	525.5	51.4	188	4	AAE11761 Rat mast
8	431	42.1	99	2	AAW88267 Human MAF
9	370.5	36.2	114	2	AAE77472 Partial s
10	306.5	30.0	70	2	AAW88266 Human MAF
11	217	21.2	35	4	AAE14192 Peptide #
12	217	21.2	35	4	ABE33139 Peptide #
13	217	21.2	35	4	AAE26602 Peptide #
14	217	21.2	35	4	ABE27967 Human pep
15	217	21.2	35	4	ABE18604 Protein #
16	217	21.2	35	4	AAW66323 Human bon
17	217	21.2	35	4	AAW53935 Human bra
18	217	21.2	35	4	ABG47989 Human liv
19	217	21.2	35	4	AAW01928 Peptide #
20	217	21.2	35	5	ABG35971 Human pep
21	216.5	21.2	182	4	AAU19660 Human nov
22	216.5	21.2	182	5	ABP47880 Human pol
23	216.5	21.2	182	7	ADC10842 Human ext
24	196.5	19.2	179	2	AAW64791 Human Kp4
25	196.5	19.2	179	2	AAW40222 CD94. 7/1

ALIGNMENTS

RESULT 1
AAW88265
ID AAW88265 standard; protein; 189 AA.
XX
AC AAW88265;
XX
DT 29-MAR-1999 (first entry)
XX
DE Human mast cell function-associated antigen (MAFA).
XX
KW Mast cell function-associated antigen; MAFA; splice variant; human;
KW inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
XX
OS Homo sapiens.

Key Location/Qualifiers
Peptide 7..10
Modified-site /note= "ITIM motif"
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site /note= "Asn is N-glycosylated"

WC9854209-A2.

03-DEC-1998.

29-MAY-1998; 98WO-GB001572.

31-MAY-1997; 97GB-00011148.

(PEPT-) PEPTIDE THERAPEUTICS LTD.

Hewitt EL, Lamers MBAC, Lamont A, Williams DH;

WPI; 1999-059806/05.

N-PSDB; AAW84198.

New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth.
Disclosure; Fig 1; 44pp; English.

XX This is the amino acid sequence of human mast cell function- associated
 CC antigen (MAFA), a type II membrane glycoprotein. cDNA (see AA984198)
 CC encoding human MAFA can be obtained from myelogenous leukaemic cell line
 CC K0812 or cDNA derived from human lung tissue. The encoded protein is
 CC similar to the rat form (see AA98277) having an intracellular domain
 CC containing a putative immunoreceptor tyrosine activation motif (ITAM) and
 CC an extracellular lectin-like domain. 2 Alternatively spliced forms (see
 CC AA98266-67) of human MAFA have been identified. Polypeptides and
 CC synthetic peptides (see AA98258-64) based on these truncated MAFA
 CC proteins can be used in methods for the treatment of inflammatory and
 CC allergic diseases, and tumour growth
 XX

XX Sequence 189 AA;
 Query Match 100.0%; Score 1023; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 1.8e-98;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTDVSIYMLELPTATQAQNDYGPQKSSSKSPSCSLVAITGLLTAVLLSVLLYQWIL 60
 DB 1 MTDVSIYMLELPTATQAQNDYGPQKSSSKSPSCSLVAITGLLTAVLLSVLLYQWIL 60
 QY 61 CQGSNYSTCASCPCDRWVKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120
 DB 61 CQGSNYSTCASCPCDRWVKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120
 QY 121 LLQVFLSEAFWCWIGLRNNSGWRWEDGSPFNFSRISSNSFVOTCGAINKNGLOASSCEVPL 180
 DB 121 LLQVFLSEAFWCWIGLRNNSGWRWEDGSPFNFSRISSNSFVOTCGAINKNGLOASSCEVPL 180
 QY 181 HGVCCKVRL 189
 DB 181 HGVCCKVRL 189

RESULT 2
 AAEL1759
 ID AAEL1759 standard; protein; 189 AA.
 AC AAEL1759;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human mast cell function associated antigen (MAFA) protein.
 XX
 KW Human; pharmaceutical composition; mast cell function associated antigen;
 KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
 KW immunosuppressive; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200170805-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 16-MAR-2001; 2001WO-US008596.
 XX
 PR 17-MAR-2000; 2000US-0190716P.
 XX
 FA (GEMI-) GEMINI SCI INC.
 XX
 PI Takahashi N, Mikayama T;
 XX
 DR WPI; 2001-611482/70.
 DR N-PSDB; AAD18734.
 XX
 PT Pharmaceutical composition for treating tumor by stimulating cytotoxic
 PT activity of natural killer cell or T-cell, comprises an agent that binds
 PT to mast cell function-associated antigen ligand on target cell.
 XX
 PS Claim 10; Page 18; 49pp; English.
 XX

CC The present invention relates to a pharmaceutical composition comprising
 CC an agent which specifically binds to a mast cell function associated
 CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
 CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
 CC ligand and a pharmaceutically acceptable excipient. The invention is
 CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
 CC binding to a ligand on a target cell, by contacting the pharmaceutical
 CC composition in vitro, ex vivo or in vivo by administering the composition
 CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
 CC on the target cell. The agent or the composition is useful for treating a
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
 CC tumour cell. The invention is also useful for inhibiting an activity of
 CC NK cell or a T-cell. The present sequence is human MAFA protein
 XX

XX Sequence 189 AA;
 Query Match 100.0%; Score 1023; DB 4; Length 189;
 Best Local Similarity 100.0%; Pred. No. 1.8e-98;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTDVSIYMLELPTATQAQNDYGPQKSSSKSPSCSLVAITGLLTAVLLSVLLYQWIL 60
 DB 1 MTDVSIYMLELPTATQAQNDYGPQKSSSKSPSCSLVAITGLLTAVLLSVLLYQWIL 60
 QY 61 CQGSNYSTCASCPCDRWVKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120
 DB 61 CQGSNYSTCASCPCDRWVKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120
 QY 121 LLQVFLSEAFWCWIGLRNNSGWRWEDGSPFNFSRISSNSFVOTCGAINKNGLOASSCEVPL 180
 DB 121 LLQVFLSEAFWCWIGLRNNSGWRWEDGSPFNFSRISSNSFVOTCGAINKNGLOASSCEVPL 180
 QY 181 HGVCCKVRL 189
 DB 181 HGVCCKVRL 189

RESULT 3
 ADD25635
 ID ADD25635 standard; protein; 189 AA.
 AC ADD25635;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Binding domain-immunoglobulin fusion protein-associated protein #95.
 XX
 KW Binding domain; immunoglobulin; fusion protein; cytostatic;
 KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
 KW neuroprotective; hinge region; immunoglobulin heavy chain;
 KW CH2 constant region; CH3 constant region; IgG1;
 KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
 KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
 KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
 KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
 XX
 OS Unidentified.
 XX
 PN US2003118592-A1.
 XX
 PD 26-JUN-2003.
 XX
 PR 25-JUL-2002; 2002US-00207655.
 XX
 PR 17-JAN-2001; 2001US-0367358P.
 PR 17-JAN-2002; 2002US-00059530.
 PR 03-JUN-2002; 2002US-0385691P.
 XX
 PA (GENE-) GENE-CRAFT INC.
 XX
 PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;

XX WPI; 2003-801317/75.

XX New binding domain-immunoglobulin fusion protein, useful for treating a

PT subject having or suspected of having a malignant condition or a B-cell

PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.

PS Disclosure; SEQ ID NO 196; 157pp; English.

XX The invention relates to a binding domain-immunoglobulin fusion protein

CC comprising a binding domain polypeptide that is fused to an

CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain

CC CH2 constant region polypeptide that is fused to the hinge region

CC polypeptide, and an immunoglobulin heavy chain CH3 constant region

CC polypeptide that is fused to the CH2 constant region polypeptide. The

CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin

CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge

CC region polypeptide, derived from (a) having 3 or more cysteine residues;

CC where the mutated human IgG1 immunoglobulin hinge region polypeptide

CC contains 2 cysteine residues, where the first cysteine is not mutated; a

CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from

CC (a) having 3 or more cysteine residues, where the mutated human IgG1

CC immunoglobulin hinge region polypeptide contains no more than one

CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region

CC polypeptide, derived from (a) having 3 or more cysteine residues; where

CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains

CC no cysteine residues. The binding domain-immunoglobulin fusion protein is

CC capable of at least one immunological activity comprising antibody

CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The

CC binding domain polypeptide is capable of specifically binding to an

CC antigen. Also included are an isolated polynucleotide encoding the

CC binding domain-immunoglobulin fusion protein, a recombinant expression

CC construct comprising the polynucleotide (operably linked to a promoter),

CC a host cell transformed or transfected with a recombinant expression

CC construct, producing the binding domain-immunoglobulin fusion protein, a

CC pharmaceutical composition comprising the binding domain-immunoglobulin

CC fusion protein or polynucleotide and a carrier, and treating a subject

CC having or suspected of having a malignant condition or a B-cell disorder.

CC The binding domain-immunoglobulin fusion protein is useful for treating a

CC subject having or suspected of having a malignant condition or a B-cell

CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,

CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple

CC sclerosis or autoimmune disease. The present sequence is a binding domain

CC -immunoglobulin fusion protein-associated protein sequence. Note: The

CC sequence data for this patent formed part of the printed specification

CC and is also available in electronic format directly from USPTO at

CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not

CC identified the sequences in the printed specification by their SEQ ID

CC number therefore none of the sequences can be explicitly identified.

XX

SQ Sequence 189 AA;

Query Match 98.4%; Score 1007; DB 7; Length 189;

Best Local Similarity 98.4%; Pred. No. 8.5e-97;

Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDVSYLMLEPTATQANDYGPQOKSSSPSCSLVAITLGLLTAVLLSVLYQWIL 60

DB 1 MTDVSYLMLEPTATQANDYGPQOKSSSPSCSLVAITLGLLTAVLLSVLYQWIL 60

QY 61 CGGSNYSTCASCPCPDRAWKMGNYHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120

DB 61 CGGSNYSTCASCPCPDRAWKMGNYHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120

QY 121 LLQVFLSEAFWIGLRNNSGWRWEDGSPNFSRISNSFVQTCCGINKNGLOASSCEVPL 180

DB 121 LLQVFLSEAFWIGLRNNSGWRWEDGSPNFSRISNSFVQTCCGINKNGLOASSCEVPL 180

QY 181 HGVCCKVRL 189

DB 181 HWVCCKVRL 189

RESULT 4

AAE11760

ID AAE11760 standard; protein; 188 AA.

XX

AC AAE11760;

XX

DT 18-DEC-2001 (first entry)

XX

DE Mouse mast cell function associated antigen (MAFA) protein.

XX

KW Mouse; pharmaceutical composition; mast cell function associated antigen;

KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;

KW immunosuppressive; cytostatic.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT Domain 64..188

FT /note="Extracellular domain"

XX

PN WO200170805-A2.

XX

PD 27-SEP-2001.

XX

PF 16-MAR-2001; 2001WO-US008596.

XX

PR 17-MAR-2000; 2000US-0190716P.

XX

PA (GEMI-) GEMINI SCI INC.

XX

PI Takahashi N, Mikayama T;

XX

DR WPI; 2001-611482/70.

DR N-PSDB; AAD18735.

XX

PT Pharmaceutical composition for treating tumor by stimulating cytotoxic

PT activity of natural killer cell or T-cell, comprises an agent that binds

PT to mast cell function-associated antigen ligand on target cell.

XX

PS Example 1; Page 19; 49pp; English.

XX

CC The present invention relates to a pharmaceutical composition comprising

CC an agent which specifically binds to a mast cell function associated

CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural

CC killer (NK)- or T-cell-expressed cell surface MAFA from binding to MAFA

CC ligand and a pharmaceutically acceptable excipient. The invention is

CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA

CC binding to a ligand on a target cell, by contacting the pharmaceutical

CC composition in vitro, ex vivo or in vivo by administering the composition

CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in

CC an amount sufficient to inhibit cell surface MAFA binding to the ligand

CC on the target cell. The agent or the composition is useful for treating a

CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic

CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible

CC tumour cell. The invention is also useful for inhibiting an activity of

CC NK cell or a T-cell. The present sequence is mouse MAFA protein

XX

SQ Sequence 188 AA;

Query Match 53.6%; Score 548.5; DB 4; Length 188;

Best Local Similarity 55.6%; Pred. No. 6.7e-49;

Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 MTDVSYLMLEPTATQANDYGPQOKSSSPSCSLVAITLGLLTAVLLSVLYQWIL 60

DB 1 MADSSIIYTLPEAPQVQDESRLKXAVLHRLPHLSRFAMVALGLLTAVLLSVLYQWIL 60

QY 61 CGGSNYSTCASCPCPDRAWKMGNYHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120

DB 61 CGGSNDSTCSHPCSPILWTRNGSHCYFVSMEKKDWNSSLKFCADKGSLLTTFPDNQGVK 120

QY 121 LLQVFLSEAFWIGLRNNSGWRWEDGSPNFSRISNSFVQTCCGINKNGLOASSCEVPL 180

Db 121 LFGYILQDFYWGILRNDGWRWGGPALSU-RILTNSLIQRCGAIHRNGLOASSCEVAL 179
 QY 181 HGUCKV 187
 :|||
 Db 180 QWICKV 186

RESULT 5

AAR77033
 ID AAR77033 standard; protein; 188 AA.

XX AC AAR77033;
 XX DT 01-FEB-1996 (first entry)
 XX DE Mammalian mast cell function-associated antigen (MAFA).

XX KW Mast cell function-associated antigen; MAFA; soluble; ligand;
 KW identification; screening; inflammation; inflammatory; allergy; allergic;
 KW prevention.

XX OS Rattus rattus.

XX PN WO9527734-A1.

XX PD 19-OCT-1995.

XX PF 06-APR-1995; 95WO-US004258.

XX PR 08-APR-1994; 94IL-00109257.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PE (RYCU/) RYCUS A.

XX PI Pecht I, Guthmann MD, Tal M;

XX DR WPI; 1995-366356/47.

XX DR N-PSDB; AAT01471.

XX PT Novel DNA encoding a mast cell function-associated antigen (MAFA) -
 PT useful for screening for ligands of MAFA which are useful for prevention
 PT of inflammatory and allergic reactions.

XX PS Claim 12; Page 37; 54pp; English.

XX CC A soluble form of mast cell function-associated antigen (MAFA) can be
 CC produced by recombinant techniques for use in the ligand- screening
 CC assay. The ligands that are identified may be used alone or in
 CC combination with the MAFA to prevent inflammatory and allergic reactions

XX SQ Sequence 188 AA;

Query Match 51.4%; Score 525.5; DB 2; Length 188;
 Best Local Similarity 53.5%; Pred. No. 1.7e-46;
 Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MTDSVIYMLPTATQANDYGPQKSSSKSCSLVAITLGLTAVLLSVLLYQWIL 60

Db 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHPCVSYLVVMVALGLLTIVILMSLLYQRTL 60

QY 61 CQGSNYSTCASCPCPDPMKYNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNEMS 120

Db 61 CCGSKGFWCQSCRCPNLWNRNGSHCYFVSMEKRDWNSSLKFCADKGSLLTFPDNQVN 120

QY 121 LLQVFLSEAFCTWIGLRNNSGWRWEDGSPLNFSRISNSSFVQTCGAINKNGLOASSCEVPL 180

Db 121 LFQEVGDFWIGLRIDGWRWEDGSPALSUS-ILSNVSVQKCGTIHRCGLHASSCEVAL 179

QY 181 HGUCKV 187

Db 180 QWICEV 186

RESULT 6

AAW88277
 ID AAW88277 standard; protein; 188 AA.

XX AC AAW88277;

XX DT 29-MAR-1999 (first entry)

XX DE Rat mast cell function-associated antigen (MAFA).

XX KW Mast cell function-associated antigen; MAFA; splice variant; rat;
 KW inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.

XX OS Rattus sp.

XX FH Key Location/Qualifiers

FT Modified-site 82..84

FT /note= "Asn is N-glycosylated"

FT Modified-site 97..99

FT /note= "Asn is N-glycosylated"

XX PN WO9854209-A2.

XX PD 03-DEC-1998.

XX PF 29-MAY-1998; 98WO-GB001572.

XX PR 31-MAY-1997; 97GB-00011148.

XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX PI Hewitt EL, Lamers MBAC, Lamont A, Williams DH;

XX DR WPI; 1999-059806/05.

XX DR N-PSDB; AAV84222.

XX PT New polypeptide having a sequence corresponding to human mast cell
 PT function-associated antigen - useful in forming and manufacturing
 PT pharmaceutical compositions in the treatment of inflammatory and allergic
 PT diseases, and tumour growth.

XX PS Disclosure; Fig 4; 44pp; English.

XX CC This is the amino acid sequence of rat mast cell function-associated
 CC antigen (MAFA), a type II membrane glycoprotein found on mast cells and
 CC basophils. The invention relates to cloning of the human MAFA molecule
 CC (see AAW88265) and to the discovery of splice variants (see AAW88266-67)
 CC of human MAFA that are not found in rat. Polypeptides and synthetic
 CC peptides (see AAW88258-64) based on human MAFA and human truncated MAFA,
 CC and polynucleotides encoding them, can be used in methods for the
 CC treatment of inflammatory and allergic diseases (e.g. rheumatoid
 CC arthritis and asthma), and tumour growth

XX SQ Sequence 188 AA;

Query Match 51.4%; Score 525.5; DB 2; Length 188;
 Best Local Similarity 53.5%; Pred. No. 1.7e-46;
 Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MTDSVIYMLPTATQANDYGPQKSSSKSCSLVAITLGLTAVLLSVLLYQWIL 60

Db 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHPCVSYLVVMVALGLLTIVILMSLLYQRTL 60

QY 61 CQGSNYSTCASCPCPDPMKYNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNEMS 120

Db 61 CCGSKGFWCQSCRCPNLWNRNGSHCYFVSMEKRDWNSSLKFCADKGSLLTFPDNQVN 120

QY 121 LLQVFLSEAFCTWIGLRNNSGWRWEDGSPLNFSRISNSSFVQTCGAINKNGLOASSCEVPL 180

Db 121 LFQEVGDFWIGLRIDGWRWEDGSPALSUS-ILSNVSVQKCGTIHRCGLHASSCEVAL 179

QY 181 HGUCKV 187

:|||


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Db          91 HWVCKVRL 99
| |||||
RESULT 9
AA077472
ID AAR77472 standard; protein; 114 AA.
XX
XX AC AAR77472;
XX DT 01-FEB-1996 (first entry)
XX DE
XX DE Partial sequence of mast cell function-associated antigen (MAFA).
XX KW Mast cell function-associated antigen; MAFA; soluble; ligand;
XX KW identification; screening; inflammation; inflammatory; allergy; allergic;
XX KW prevention.
XX OS Rattus rattus.
XX XX
XX PN WO9527734-A1.
XX XX
XX PD 19-OCT-1995.
XX XX
XX PF 06-APR-1995; 95WO-US004258.
XX XX
XX PR 08-APR-1994; 94IL-00109257.
XX XX
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX FA (RYCU/) RYCU A.
XX XX
XX PI Pecht I, Guthmann MD, Tal M;
XX XX
XX DR WPI; 1995-366356/47.
XX DR N-PSDB; AAT01471.
XX XX
XX PT Novel DNA encoding a mast cell function-associated antigen (MAFA) -
XX PT useful for screening for ligands of MAFA which are useful for prevention
XX PT of inflammatory and allergic reactions.
XX XX
XX PS Disclosure; Page 38; 54pp; English.
XX XX
XX CC A soluble form of mast cell function-associated antigen (MAFA) can be
XX CC produced by recombinant techniques for use in the ligand- screening
XX CC assay. The ligands that are identified may be used alone or in
XX CC combination with the MAFA to prevent inflammatory and allergic reactions
XX CC
XX SQ Sequence 114 AA;
Query Match 36.2%; Score 370.5; DB 2; Length 114;
Best Local Similarity 58.4%; Pred. No. 1.4e-30;
Matches 66; Conservative 18; Mismatches 28; Indels 1; Gaps 1;
QY 75 CPDRWKYGNHCYFYFSEVKDWNSSLEFCIARDSHLLVITDQMSLLQVFLSEAFQWIG 134
Db 1 CPNLWNRNGSHCYFYFSEVKDWNSSLEFCIARDSHLLVITDQMSLLQVFLSEAFQWIG 60
QY 135 LRNNSGWRWEDGSPINFSRISNSFVQTCGAINKNGLOASCEYPLHGVCVKV 187
Db 61 LRIDGWRWEDGPALSL-ILSNVWQKGTIHRGGLHASSCEVALQWICEKV 112
RESULT 10
AAW88266
ID AAW88266 standard; protein; 70 AA.
XX
XX AC AAW88266;
XX XX
XX DT 29-MAR-1999 (first entry)
XX DE
XX DE Human MAFA splice variant huMAFA(E3-).
XX KW Mast cell function-associated antigen; MAFA; huMAFA(E3-); splice variant;
KW human; inflammation; allergy; asthma; rheumatoid arthritis; tumour;
therapy.
KW Homo sapiens.
WO9854209-A2.
03-DEC-1998.
29-MAY-1998; 98WO-GH001572.
31-MAY-1997; 97GB-00011148.
(PBPT-) PEPTIDE THERAPEUTICS LTD.
Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
WPI; 1999-059806/05.
N-PSDB; AAV84199.
New polypeptide having a sequence corresponding to human mast cell
function-associated antigen - useful in forming and manufacturing
pharmaceutical compositions in the treatment of inflammatory and allergic
diseases, and tumour growth.
Disclosure; Fig 2; 4pp; English.
XX
XX CC This is the amino acid sequence of human mast cell function- associated
XX CC antigen (MAFA) splice variant huMAFA(E3-). huMAFA(E3-) is a major
XX CC transcript, not found in rat, but highly expressed in human lung and
XX CC granulocyte-enriched blood cells. The truncated protein includes the
XX CC intracellular and transmembrane regions of human MAFA (see AAW88265),
XX CC followed immediately by a polyproline motif (see AAW88264) due to a
XX CC reading frameshift. This unique motif has been used to design peptides
XX CC (see AAW88259-64, AAW88268-72) that inhibit T cell antigen receptor-
XX CC dependent activation induced by interleukin-2 (IL2) secretion from human
XX CC Jurkat T cells or IgE dependent degranulation of rat basophil leukaemic
XX CC cells. Inhibition of IL2 production prevents T cell proliferation and
XX CC suppresses the immune system. These peptides, truncated MAFA polypeptides
XX CC including huMAFA(E3-), and polynucleotides encoding them, can be used be
XX CC used in compositions for the treatment of inflammatory and allergic
XX CC diseases (e.g. rheumatoid arthritis and asthma), or tumour growth
XX XX
XX SQ Sequence 70 AA;
Query Match 30.0%; Score 306.5; DB 2; Length 70;
Best Local Similarity 82.9%; Pred. No. 3.5e-24;
Matches 63; Conservative 1; Mismatches 5; Indels 7; Gaps 1;
QY 1 MTDSVIYSMLELPTAQANDYGPQKSSSKSPSCSLVAITLGLTAVLLSVLLYQWIL 60
Db 1 MTDSVIYSMLELPTAQANDYGPQKSSSKSPSCSLVAITLGLTAVLLSVLLYQWIL 60
QY 61 CQGSNYSTCASCPSCP 76
Db 61 CQ-----EPAPSPFP 69
RESULT 11
AAW14192
ID AAW14192 standard; protein; 35 AA.
XX
XX AC AAW14192;
XX XX
XX DT 12-OCT-2001 (first entry)
XX DE
XX DE Peptide #626 encoded by probe for measuring cervical gene expression.
XX KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX KW cervical cancer.
XX OS Homo sapiens.
XX XX
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PN WO200157278-A2.
XX
XX
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000670.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human cervical epithelial cells.
XX
XX Claim 27; SEQ ID NO 19018; 487pp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
XX (SENP: see AAL10068-AAL28459). The present sequence is a peptide encoded
XX by one such probe. The SENPs are derived from human Hela cells. The SENPs
XX can be used to produce a single exon microarray, which can be used for
XX measuring human gene expression in a sample derived from human cervical
XX epithelial cells. By measuring gene expression, the probes are therefore
XX useful in grading and/or staging of diseases of the cervix, notably
XX cervical cancer. Note: The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 35 AA;
XX
XX Query Match 21.2%; Score 217; DB 4; Length 35;
XX Best Local Similarity 100.0%; Pred. No. 3.1e-15;
XX Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 64 SNYSTCASCPCPDRMKYGNHCYFVSVEEKDWS 98
XX 1 SNYSTCASCPCPDRMKYGNHCYFVSVEEKDWS 35
XX
XX RESULT 12
XX ABB33139
XX ID ABB33139 standard; peptide; 35 AA.
XX
XX AC ABB33139;
XX
XX XX 04-FEB-2002 (first entry)
XX DT
XX DE Peptide #645 encoded by human foetal liver single exon probe.
XX
XX XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
XX OS Homo sapiens.
XX
XX PN WO200157277-A2.
XX
XX PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000669.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.
XX
XX Claim 27; SEQ ID NO 26871; 654pp; English.
XX
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PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human fetal liver.
XX
XX Claim 27; SEQ ID NO 25774; 639pp + Sequence Listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for measuring
XX human gene expression in a sample derived from human foetal liver. The
XX single exon nucleic acid probes may be used for predicting, measuring and
XX displaying gene expression in samples derived from human fetal liver. The
XX present sequence is a peptide encoded by a single exon nucleic acid probe
XX of the invention. Note: The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 35 AA;
XX
XX Query Match 21.2%; Score 217; DB 4; Length 35;
XX Best Local Similarity 100.0%; Pred. No. 3.1e-15;
XX Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 64 SNYSTCASCPCPDRMKYGNHCYFVSVEEKDWS 98
XX 1 SNYSTCASCPCPDRMKYGNHCYFVSVEEKDWS 35
XX
XX RESULT 13
XX AAM26602
XX ID AAM26602 standard; protein; 35 AA.
XX
XX AC AAM26602;
XX
XX XX 17-OCT-2001 (first entry)
XX DT
XX DE Peptide #639 encoded by probe for measuring placental gene expression.
XX
XX XX Probe; microarray; human; placenta; antenatal diagnosis;
XX KW genetic disorder.
XX
XX OS Homo sapiens.
XX
XX PN WO200157272-A2.
XX
XX PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.
XX
XX Claim 27; SEQ ID NO 26871; 654pp; English.
XX
```

CC The present invention relates to single exon nucleic acid probes (SENP:
CC see AA131315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 35 AA;

Query Match 21.2%; Score 217; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.1e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 SNYSTCASCPCPDPRWKKYGNHCYFVSVEEKDWS 98
|||||
Db 1 SNYSTCASCPCPDPRWKKYGNHCYFVSVEEKDWS 35

RESULT 14
ABB27967
ID ABB27967 standard; peptide; 35 AA.

XX
AC ABB27967;

DT 01-FEB-2002 (first entry)

DE Human peptide #618 encoded by breast cell single exon nucleic acid probe.
XX
KW Human; microarray; single exon probe; gene expression; breast; disease;
KW cancer.

OS Homo sapiens.

PN WO200157271-A2.

XX
PD 09-AUG-2001.

XX
PF 30-JAN-2001; 2001WO-US000662.

XX
PR 04-FEB-2000; 2000US-0180312P.

XX
PR 26-MAY-2000; 2000US-0207456P.

XX
PR 30-JUN-2000; 2000US-00608408.

XX
PR 03-AUG-2000; 2000US-00632366.

XX
PR 21-SEP-2000; 2000US-0234687P.

XX
PR 27-SEP-2000; 2000US-0236359P.

XX
PR 04-OCT-2000; 2000GB-00024263.

XX
PA (MOLE-) MOLECULAR DYNAMICS INC.

XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX
WPI; 2001-496933/54.

XX
PT New spatially-addressable set of single exon nucleic acid probes, useful
PT for measuring gene expression in sample derived from human breast,
PT comprises number of single exon nucleic acid probes.

XX
PS Claim 27; SEQ ID NO 10935; 327pp + Sequence Listing; English.

XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting the
CC probes with a collection of detectably labelled nucleic acids derived
CC from mRNA of human breast, and then measuring the label bound to each
CC probe of the microarray. The probes are useful for verifying the
CC expression of regions of genomic DNA predicted to encode proteins. They
CC are useful for gene discovery, and for determining predisposition and/or
CC prognosing breast disease. Gene expression analysis is useful for
CC assessing the toxicity of chemical agents on cells. The microarray of
CC this invention presents a far greater diversity of probes for measuring
CC gene expression, with far less bias than expressed sequence tag
CC microarrays. The method is suitable for rapid production of functional
CC information from genomic sequence. The present sequence is a peptide

CC encoded by a single exon nucleic acid probe of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 35 AA;

Query Match 21.2%; Score 217; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.1e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 SNYSTCASCPCPDPRWKKYGNHCYFVSVEEKDWS 98
|||||
Db 1 SNYSTCASCPCPDPRWKKYGNHCYFVSVEEKDWS 35

RESULT 15
ABB18604
ID ABB18604 standard; protein; 35 AA.

XX
AC ABB18604;

DT 23-JAN-2002 (first entry)

DE Protein #603 encoded by probe for measuring heart cell gene expression.

XX
KW Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.

XX
OS Homo sapiens.

PN WO200157274-A2.

XX
PD 09-AUG-2001.

XX
PF 30-JAN-2001; 2001WO-US000666.

XX
PR 04-FEB-2000; 2000US-0180312P.

XX
PR 26-MAY-2000; 2000US-0207456P.

XX
PR 30-JUN-2000; 2000US-00608408.

XX
PR 03-AUG-2000; 2000US-00632366.

XX
PR 21-SEP-2000; 2000US-0234687P.

XX
PR 27-SEP-2000; 2000US-0236359P.

XX
PR 04-OCT-2000; 2000GB-00024263.

XX
PA (MOLE-) MOLECULAR DYNAMICS INC.

XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX
WPI; 2001-488899/53.

XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.

XX
PS Claim 15; SEQ ID NO 20374; 530pp; English.

XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 35 AA;

Query Match

21.2%; Score 217; DB 4; Length 35;

Best Local Similarity 100.0%; Pred. No. 3.1e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 SNYSTCASCPCPDRAWMKYGNHCYFVSVEEKDWS 98
|||||
Db 1 SNYSTCASCPCPDRAWMKYGNHCYFVSVEEKDWS 35
|||||

Search completed: August 10, 2004, 16:33:40
Job time : 54 secs

This Page Blank (uspto)

..... (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:35:05 ; Search time 53 Seconds

(without alignments)
1118.605 Million cell updates/sec

Title: US-09-811-367B-1

Perfect score: 1023

Sequence: 1 MTDSVIYMLELPTAQON.....GLQASSCEVPLGVCKKVR 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 727970

Minimum DB seq length: 0

Maximum DB seq length: 189

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09C_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1023	100.0	189	9	US-09-811-367B-1
2	1007	98.4	189	14	US-10-207-655-196
3	548.5	53.6	188	9	US-09-811-367B-3
4	525.5	51.4	188	9	US-09-811-367B-5
5	217	21.2	35	9	US-09-864-761-33902
6	216.5	21.2	182	9	US-09-764-870-310
7	216.5	21.2	182	14	US-10-125-540-310
8	196.5	19.2	179	10	US-09-919-039-130
9	196.5	19.2	179	15	US-10-335-009-10
10	175	17.1	149	10	US-09-284-320-11
11	175	17.1	149	13	US-10-114-893-32
12	175	17.1	149	14	US-10-088-859-2
13	175	17.1	149	14	US-10-179-528-1
14	168.5	16.5	95	12	US-10-424-599-222182
15	168	16.4	149	9	US-09-944-807-6

16	168	16.4	149	15	US-10-335-009-6	Sequence 6, Appli
17	166	16.2	133	12	US-10-239-656-3	Sequence 3, Appli
18	166	16.2	143	12	US-10-239-656-2	Sequence 2, Appli
19	166	16.2	162	12	US-10-239-656-90	Sequence 90, Appli
20	165	16.1	140	9	US-09-764-870-340	Sequence 340, App
21	165	16.1	140	9	US-09-764-870-486	Sequence 486, App
22	165	16.1	140	14	US-10-125-540-340	Sequence 340, App
23	165	16.1	140	14	US-10-125-540-486	Sequence 486, App
24	165	16.1	189	9	US-09-764-870-487	Sequence 487, App
25	165	16.1	189	14	US-10-125-540-487	Sequence 487, App
26	163.5	16.0	94	9	US-09-764-870-466	Sequence 466, App
27	163.5	16.0	94	14	US-10-125-540-466	Sequence 466, App
28	162.5	15.9	165	10	US-09-759-130B-98	Sequence 98, Appli
29	162.5	15.9	165	16	US-10-741-790-98	Sequence 98, Appli
30	161	15.7	162	14	US-10-270-470-2	Sequence 2, Appli
31	161	15.7	181	13	US-10-114-893-22	Sequence 22, Appli
32	159.5	15.6	165	12	US-10-262-839-76	Sequence 76, Appli
33	159	15.5	187	14	US-10-212-198-9	Sequence 9, Appli
34	159	15.5	187	14	US-10-212-198-10	Sequence 10, Appli
35	159	15.5	188	10	US-09-759-130B-83	Sequence 83, Appli
36	159	15.5	188	16	US-10-741-790-83	Sequence 83, Appli
37	158.5	15.5	124	12	US-09-964-956-67	Sequence 67, Appli
38	158.5	15.5	124	12	US-10-072-012-836	Sequence 836, App
39	158.5	15.5	137	14	US-10-106-698-5855	Sequence 4, Appli
40	157.5	15.4	132	15	US-10-335-009-4	Sequence 836, App
41	157.5	15.4	145	10	US-09-759-130B-108	Sequence 108, App
42	157.5	15.4	145	16	US-10-741-790-108	Sequence 108, App
43	157	15.3	146	12	US-10-296-115-1275	Sequence 1275, Ap
44	155.5	15.2	143	9	US-09-764-870-471	Sequence 471, App
45	155.5	15.2	143	14	US-10-125-540-471	Sequence 471, App

ALIGNMENTS

RESULT 1

US-09-811-367B-1
; Sequence 1, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No, US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THE
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-367B-1

Query Match 100.0%; Score 1023; DB 9; Length 189;
Best Local Similarity 100.0%; Pred. No. 3.5e-97;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTDSVIYMLELPTAQNDYGPQKSSKSPSCSLVAITLGLTAVLLSVLLYQWIL	60
DB	1	MTDSVIYMLELPTAQNDYGPQKSSKSPSCSLVAITLGLTAVLLSVLLYQWIL	60
QY	61	COGSNYSTCASCPDRWKYGNHCYFVSBEKDNSSLEFCCLARDSHLLVITDNQMS	120
DB	61	COGSNYSTCASCPDRWKYGNHCYFVSBEKDNSSLEFCCLARDSHLLVITDNQMS	120
QY	121	LLQVFLSEAFWIGLRNNSGWEDGSPINFRISSNSFVQTCGAINKNGLASCEVPL	180
DB	121	LLQVFLSEAFWIGLRNNSGWEDGSPINFRISSNSFVQTCGAINKNGLASCEVPL	180

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QY 181 HGVCCKVRL 189
Db 181 HGVCCKVRL 189

RESULT 2
US-10-207-655-196
; Sequence 196, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 196
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-196

Query Match 98.4%; Score 1007; DB 14; Length 189;
Best Local Similarity 98.4%; Pred. No. 1.6e-95;
Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDSVIYSMLPPTATQAQNDYGPQOKSSSKPSCSCLVAITGLLTAVLLSVLLYQWIL 60
Db 1 MTDSVIYSMLPPTATQAQNDYGPQOKSSSKPSCSCLVAITGLLTAVLLSVLLYQWIL 60

QY 61 CGGSNYSTCASCPCPDRAWKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120
Db 61 CGGSNYSTCASCPCPDRAWKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120

QY 121 LLOVFLSEAFWIGLRNNSGWRWEDGSPLNFSRISNSSFVQTCGAINKNGLOASSCEVPL 180
Db 121 LLOVFLSEAFWIGLRNNSGWRWEDGSPLNFSRISNSSFVQTCGAINKNGLOASSCEVPL 180

QY 181 HGVCCKV 187
Db 180 QWICEKV 186

RESULT 3
US-09-811-367B-3
; Sequence 3, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-811-367B-3

Query Match 53.6%; Score 548.5; DB 9; Length 188;
Best Local Similarity 55.6%; Pred. No. 2.9e-48;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 181 HGVCCKVRL 189
Db 181 HWVCCKVRL 189

RESULT 3
US-09-811-367B-3
; Sequence 3, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-811-367B-3

Query Match 51.4%; Score 525.5; DB 9; Length 188;
Best Local Similarity 53.5%; Pred. No. 6.7e-46;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

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QY 61 CGGSNYSTCASCPCPDRAWKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120
Db 61 CGGSNYSTCASCPCPDRAWKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120

QY 121 LLOVFLSEAFWIGLRNNSGWRWEDGSPLNFSRISNSSFVQTCGAINKNGLOASSCEVPL 180
Db 121 LLOVFLSEAFWIGLRNNSGWRWEDGSPLNFSRISNSSFVQTCGAINKNGLOASSCEVPL 180

QY 181 HGVCCKV 187
Db 180 QWICEKV 186

RESULT 5
US-09-864-761-33902
; Sequence 33902, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
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; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33902
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 8.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 18
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 22
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 30
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 6.1
; OTHER INFORMATION: EST HUMAN HIT: BF241894.1, EVALUE 4.00e-15
; OTHER INFORMATION: EST HUMAN HIT: AA188327.1, EVALUE 1.00e-14
; OTHER INFORMATION: SWISSPROT HIT: P14370, EVALUE 3.00e-04
US-09-864-761-33902

Query Match 21.2%; Score 217; DB 9; Length 35;
Best Local Similarity 100.0%; Pred. No. 5.3e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 SNYSTCASCPCPDRWMKYGNHCYFVSVEEKDWS 98
Db 1 SNYSTCASCPCPDRWMKYGNHCYFVSVEEKDWS 35

RESULT 6
US-09-764-870-310
; Sequence 310, Application US/09764870
; Publication No. US20030108871A1

; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 310
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-310

Query Match 21.2%; Score 216.5; DB 9; Length 182;
Best Local Similarity 35.0%; Pred. No. 4.6e-14;
Matches 48; Conservative 22; Mismatches 48; Indels 19; Gaps 5;

QY 64 SNYSTCASCPCS-----CPDRWMKYGNHCYFVSVEEKDWSLSLEFCLARDSHLLVITDQOE 118
Db 49 SNKDLCASRSADQTVLCQSEWLKYGKCYWFSNEMKSWSDSYVYCLERKSHLLIHDQLE 108

QY 119 MSLLQVFLSEA-FCWIGLRNNS---GWRWEDGSPINFRSSNSFVQ-----TCGAINK 168
Db 109 MAFIQKNLRQLNYVWIGLNFSLKMTWTWVDGSPID----SKIFFIKGPAKENSAAAIKE 164

QY 169 NGLQASSCEVPLHGVC 185
Db 165 SKIFSETCSSVFKWICQ 181

RESULT 7
US-10-125-540-310
; Sequence 310, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214C1
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 310
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-540-310

Query Match 21.2%; Score 216.5; DB 14; Length 182;
Best Local Similarity 35.0%; Pred. No. 4.6e-14;
Matches 48; Conservative 22; Mismatches 48; Indels 19; Gaps 5;

QY 64 SNYSTCASCPCS-----CPDRWMKYGNHCYFVSVEEKDWSLSLEFCLARDSHLLVITDQOE 118
Db 49 SNKDLCASRSADQTVLCQSEWLKYGKCYWFSNEMKSWSDSYVYCLERKSHLLIHDQLE 108

QY 119 MSLLQVFLSEA-FCWIGLRNNS---GWRWEDGSPINFRSSNSFVQ-----TCGAINK 168
Db 109 MAFIQKNLRQLNYVWIGLNFSLKMTWTWVDGSPID----SKIFFIKGPAKENSAAAIKE 164

QY 169 NGLQASSCEVPLHGVC 185
Db 165 SKIFSETCSSVFKWICQ 181

RESULT 8
US-09-919-039-130
; Sequence 130, Application US/09919039
; Publication No. US20030108871A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 130
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 516300CDI
US-09-919-039-130

Query Match      19.2%; Score 196.5; DB 10; Length 179;
Best Local Similarity 32.7%; Pred. No. 5.2e-12;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCLAIVTGLTAVLLSVLLQWILCOGSN--YSTCASCPCSPDRWMKYGNGHCYFVSVE 92
DB 20 CLSLMA-TLGIILKNSFTKLIEPAFTPGPNIELQKSDCCSQEKWVGRCNCYFISSE 78
QY 93 EKDNSSLEFCLARDSHLLVITDNOEMSLLOVFLSEAFQWIGL---RNNSGRWEDGSP 149
DB 79 QKTWNSRHLCASQKSSLLQNTDELDFMS--SSQQFYWIGLSYSEEHATWLWENGSA 136
QY 150 NFRSISNSF-----VOTCGAINKNG-LQASSCEVPLHGVCCK 186
DB 137 --SQYLPSPETENTKNCIAYNPNGNALDESCEDKKNRYICKQ 176

RESULT 9
US-10-335-009-10
; Sequence 10, Application US/10335009
; Publication No. US20040001804A1
; GENERAL INFORMATION:
; APPLICANT: Boles, Kent S.
; APPLICANT: Portunelloor, Mathew A.
; TITLE OF INVENTION: LLT USES THEREOF IN IMMUNE SYSTEM MODULATION
; FILE REFERENCE: 11707.02/469887-7
; CURRENT APPLICATION NUMBER: US/10/335,009
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US 09/475,365
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-009-10

Query Match      19.2%; Score 196.5; DB 15; Length 179;
Best Local Similarity 32.7%; Pred. No. 5.2e-12;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCLAIVTGLTAVLLSVLLQWILCOGSN--YSTCASCPCSPDRWMKYGNGHCYFVSVE 92
DB 20 CLSLMA-TLGIILKNSFTKLIEPAFTPGPNIELQKSDCCSQEKWVGRCNCYFISSE 78
QY 93 EKDNSSLEFCLARDSHLLVITDNOEMSLLOVFLSEAFQWIGL---RNNSGRWEDGSP 149
DB 79 QKTWNSRHLCASQKSSLLQNTDELDFMS--SSQQFYWIGLSYSEEHATWLWENGSA 136
QY 150 NFRSISNSF-----VOTCGAINKNG-LQASSCEVPLHGVCCK 186
DB 137 --SQYLPSPETENTKNCIAYNPNGNALDESCEDKKNRYICKQ 176

; GENERAL INFORMATION:
; APPLICANT: Kato, Seishi et al.
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs
; TITLE OF INVENTION: ENCODING THESE PROTEINS
; FILE REFERENCE: GIN-6705CFUS
; CURRENT APPLICATION NUMBER: US/09/284,320
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: JP 8-301429
; PRIOR FILING DATE: 1996-11-13
; PRIOR APPLICATION NUMBER: PCT/JP97/04056
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-284-320-11

Query Match      17.1%; Score 175; DB 10; Length 149;
Best Local Similarity 32.2%; Pred. No. 6.8e-10;
Matches 37; Conservative 24; Mismatches 48; Indels 6; Gaps 3;

QY 75 CPDRWMKYGNGHCYFVSVEEKDNSSLEFCLARDSHLLVITDNOEMSLLOVFLSEAFQWIG 134
DB 35 CPYDWIGFQNKCYFYSKEEGDNSSKYNCSSTQHADTLTIDNIEWNFJRRYKCSDDHWIG 94
QY 135 L---RNNSGRWEDGSPNLSFRISNSVQTCGAINKNGLOASSCEVPLHGVCCK 186
DB 95 LKMAKNRTG-QWVDOA--TFYKSGMRGSGCAYLSDGATARTCYTERKWKCR 146

RESULT 11
US-10-114-893-32
; Sequence 32, Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Meirberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Carlin-Duckett, McKeough
; APPLICANT: Kelleher, Kerry S.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6000-10A
; CURRENT APPLICATION NUMBER: US/10/114,893
; CURRENT FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; EARLIER FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-893-32

Query Match      17.1%; Score 175; DB 13; Length 149;
Best Local Similarity 32.2%; Pred. No. 6.8e-10;
Matches 37; Conservative 24; Mismatches 48; Indels 6; Gaps 3;

QY 75 CPDRWMKYGNGHCYFVSVEEKDNSSLEFCLARDSHLLVITDNOEMSLLOVFLSEAFQWIG 134
```

```

; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 130
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 516300CDI
US-09-919-039-130

Query Match      19.2%; Score 196.5; DB 10; Length 179;
Best Local Similarity 32.7%; Pred. No. 5.2e-12;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCLAIVTGLTAVLLSVLLQWILCOGSN--YSTCASCPCSPDRWMKYGNGHCYFVSVE 92
DB 20 CLSLMA-TLGIILKNSFTKLIEPAFTPGPNIELQKSDCCSQEKWVGRCNCYFISSE 78
QY 93 EKDNSSLEFCLARDSHLLVITDNOEMSLLOVFLSEAFQWIGL---RNNSGRWEDGSP 149
DB 79 QKTWNSRHLCASQKSSLLQNTDELDFMS--SSQQFYWIGLSYSEEHATWLWENGSA 136
QY 150 NFRSISNSF-----VOTCGAINKNG-LQASSCEVPLHGVCCK 186
DB 137 --SQYLPSPETENTKNCIAYNPNGNALDESCEDKKNRYICKQ 176

RESULT 9
US-10-335-009-10
; Sequence 10, Application US/10335009
; Publication No. US20040001804A1
; GENERAL INFORMATION:
; APPLICANT: Boles, Kent S.
; APPLICANT: Portunelloor, Mathew A.
; TITLE OF INVENTION: LLT USES THEREOF IN IMMUNE SYSTEM MODULATION
; FILE REFERENCE: 11707.02/469887-7
; CURRENT APPLICATION NUMBER: US/10/335,009
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US 09/475,365
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-009-10

Query Match      19.2%; Score 196.5; DB 15; Length 179;
Best Local Similarity 32.7%; Pred. No. 5.2e-12;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCLAIVTGLTAVLLSVLLQWILCOGSN--YSTCASCPCSPDRWMKYGNGHCYFVSVE 92
DB 20 CLSLMA-TLGIILKNSFTKLIEPAFTPGPNIELQKSDCCSQEKWVGRCNCYFISSE 78
QY 93 EKDNSSLEFCLARDSHLLVITDNOEMSLLOVFLSEAFQWIGL---RNNSGRWEDGSP 149
DB 79 QKTWNSRHLCASQKSSLLQNTDELDFMS--SSQQFYWIGLSYSEEHATWLWENGSA 136
QY 150 NFRSISNSF-----VOTCGAINKNG-LQASSCEVPLHGVCCK 186
DB 137 --SQYLPSPETENTKNCIAYNPNGNALDESCEDKKNRYICKQ 176
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Db 35 CPYDWIGFQNKCYFYSKEEGDWNSKYNCSQHADLTIIDNIEEMFLRRYKCSSDHWIG 94
QY 135 L---RNNSGWRWEDGSPLNFSRISNSFVQTCGAINKNGLOASSCEVPLHGVCKK 186
Db 95 LKMAKNRTG-QWVDGA--TFTKSGMRGSGCAYLSDDGAATARCCTYTERKWICKR 146

RESULT 12
US-10-088-859-2
; Sequence 2, Application US/10088859
; Publication No. US2003014846A1
; GENERAL INFORMATION:
; APPLICANT: KATO, Seiichi
; APPLICANT: NAGATA, Naoki
; APPLICANT: FUJIMURA, Naoko
; APPLICANT: KOBAYASHI, Midori
; APPLICANT: ITO, Koichi
; APPLICANT: ISHIZUKA, Yoshiko
; TITLE OF INVENTION: A Method for Producing an Antibody by Gene Immunization
; FILE REFERENCE: 2002-0400A/LC/00653
; CURRENT APPLICATION NUMBER: US/10/088,859
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: PCT/JP01/06371
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: JP2000-222743
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: JP2000-254407
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 2
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-088-859-2

Query Match 17.1%; Score 175; DB 14; Length 149;
Best Local Similarity 32.2%; Pred. No. 6.8e-10;
Matches 37; Conservative 24; Mismatches 48; Indels 6; Gaps 3;

QY 75 CPDRWKYGNHCYFYSVEEKDWNSLFLCLARDSHLLVITDQMSLLQVFLSEAFCWIG 134
Db 35 CPYDWIGFQNKCYFYSKEEGDWNSKYNCSQHADLTIIDNIEEMFLRRYKCSSDHWIG 94
QY 135 L---RNNSGWRWEDGSPLNFSRISNSFVQTCGAINKNGLOASSCEVPLHGVCKK 186
Db 95 LKMAKNRTG-QWVDGA--TFTKSGMRGSGCAYLSDDGAATARCCTYTERKWICKR 146

RESULT 13
US-10-179-528-1
; Sequence 1, Application US/10179528
; Publication No. US20030166136A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/179,528
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; FILING DATE: 24-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,523
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0281 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PITUNOT03
; CLONE: 1756224
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-179-528-1

Query Match 17.1%; Score 175; DB 14; Length 149;
Best Local Similarity 32.2%; Pred. No. 6.8e-10;
Matches 37; Conservative 24; Mismatches 48; Indels 6; Gaps 3;

QY 75 CPDRWKYGNHCYFYSVEEKDWNSLFLCLARDSHLLVITDQMSLLQVFLSEAFCWIG 134
Db 35 CPYDWIGFQNKCYFYSKEEGDWNSKYNCSQHADLTIIDNIEEMFLRRYKCSSDHWIG 94
QY 135 L---RNNSGWRWEDGSPLNFSRISNSFVQTCGAINKNGLOASSCEVPLHGVCKK 186
Db 95 LKMAKNRTG-QWVDGA--TFTKSGMRGSGCAYLSDDGAATARCCTYTERKWICKR 146

RESULT 14
US-10-424-599-222182
; Sequence 222182, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(S3223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 222182
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(95)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_4265C.1.pep
US-10-424-599-222182

Query Match 16.5%; Score 168.5; DB 12; Length 95;
Best Local Similarity 39.3%; Pred. No. 1.8e-09;
Matches 33; Conservative 16; Mismatches 26; Indels 9; Gaps 3;

QY 67 STCASCPCPDWRWKYGNHCYFYSVEEKDWNSLFLCLARDSHLLVITDQMSLLQVFL 126
Db 10 SSCA-----CLKWIRHQCSXCFISKEKSWGSGREFCASQNSLLQOTRNLFSMS--S 63
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Tue Aug 10 17:15:48 2004

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QY 127 SEAFWIGLNN---SGWRWEDGS 147
|:|||||:| | | | |
Db 64 SOAFFWIGHYNEERSXWLWEDGT 87

RESULT 15
US-09-944-807-6
; Sequence 6, Application US/09944807
; Patent No. US20020119494A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Method for identifying substances which positively
; TITLE OF INVENTION: influence inflammatory conditions of chronic
; TITLE OF INVENTION: inflammatory airway diseases
; FILE REFERENCE: 082 00n
; CURRENT APPLICATION NUMBER: US/09/944,807
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: UK 0021484.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-944-807-6

Query Match 16.4%; Score 168; DB 9; Length 149;
Best Local Similarity 31.3%; Pred. No. 3.6e-09;
Matches 36; Conservative 24; Mismatches 49; Indels 6; Gaps 3;

QY 75 CPDRWMKYNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMSLLOVFLSEAFCWIG 134
| | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 35 CPYDWIGFQNKCYFSEKEDWNSSKYNCSYQADLTITDNEENFLRYKCSSDHWIG 94
| | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 135 L---RNSGWRWEDGSPLEFNRISNFSVOTCGAINKNGLOASCEVPLHGVCKK 186
| | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 95 LKMAKNRTG-QWVHGA--TFTKSGMRGSGCAYLSDDGATARCYTEKWI CRK 146
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Search completed: August 10, 2004, 16:40:34
Job time : 55 secs

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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:32:44 ; Search time 18 Seconds
(without alignments)
542.073 Million cell updates/sec

Title: US-09-811-367B-1

Perfect score: 1023

Sequence: 1 MTDSVIYXMLELPTATQAN.....GLQASSCEVPLHGVCVKVRL 189

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 303294

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Maximum DB seq length: 189

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	525.5	51.4	188	3	US-08-722-126A-5
2	525.5	51.4	188	5	PCT-US95-04258-5
3	430	42.0	76	4	US-09-531-056A-23
4	370.5	36.2	114	3	US-08-722-126A-6
5	370.5	36.2	114	5	PCT-US95-04258-6
6	196.5	19.2	179	1	US-08-890-095-9
7	196.5	19.2	179	2	US-08-650-578-2
8	196.5	19.2	179	2	US-08-688-342-3
9	196.5	19.2	179	3	US-09-113-789-9
10	196.5	19.2	179	3	US-09-113-789-9
11	175.5	17.2	168	3	US-08-772-440-17
12	173	16.9	175	3	US-08-772-440-15
13	172	16.8	134	3	US-08-772-440-16
14	169.5	16.6	120	3	US-08-543-246B-18
15	169.5	16.6	135	3	US-08-543-246B-17
16	166	16.2	134	3	US-08-543-246B-20
17	164.5	16.1	135	3	US-08-543-246B-19
18	162	15.8	129	3	US-08-722-126A-10
19	162	15.8	129	5	PCT-US95-04258-10
20	161.5	15.8	173	4	US-09-531-056A-4
21	158.5	15.5	79	4	US-09-531-056A-19
22	158	15.4	176	3	US-08-772-440-8
23	158	15.4	180	3	US-08-772-440-31
24	156.5	15.3	77	4	US-09-531-056A-22
25	155.5	15.2	122	3	US-08-722-126A-9
26	155.5	15.2	122	5	PCT-US95-04258-9
27	155.5	15.2	187	4	US-09-127-946-12

28 155 15.2 115 3 US-08-722-126A-8
29 155 15.2 115 5 PCT-US95-04258-8
30 154 15.1 126 3 US-08-772-440-10
31 152 14.9 78 4 US-09-531-056A-15
32 152 14.9 78 4 US-09-531-056A-16
33 150 14.7 141 4 US-09-535-521-14
34 150 14.7 187 4 US-09-535-521-17
35 148 14.5 78 4 US-09-531-056A-20
36 147.5 14.4 139 4 US-09-535-521-11
37 147.5 14.4 174 2 US-08-401-530A-2
38 147.5 14.4 174 2 US-08-709-662-2
39 147.5 14.4 175 1 US-08-909-725-6
40 146.5 14.3 123 4 US-09-535-521-25
41 146 14.3 117 1 US-07-614-443A-2
42 146 14.3 117 1 US-08-294-859-2
43 146 14.3 117 1 US-08-481-676-2
44 142 13.9 77 4 US-09-531-056A-21
45 142 13.9 131 3 US-08-772-440-23

ALIGNMENTS

RESULT 1
US-08-722-126A-5
; Sequence 5, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-722-126A-5

Query Match 51.4%; Score 525.5; DB 3; Length 188;
Best Local Similarity 53.5%; Pred. No. 1.1e-48;

	Matches	100;	Conservative	29;	Mismatches	57;	Indels	1;	Gaps	17;
Qy	1	MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKFCSCSLVAITLGLLTAVLLSVLLYQWIL	60							
Db	1	MADNSIYSTLELPAAPRVQDSDRWKVKAVLHRPCVSYLVVMVALGULLTIVMLSLLYQRTL	60							
Qy	61	COGSNYTCASCPSCPPORWVKYGNHCYFFSVEEKDWNSSLEFCLARDSHLLVITTDQEMS	120							
Db	61	CCGSKGPMCSQCSPCLMLWRNGSHCYFFSMEKEDWNSSLKFCADKGSHLLTTFPDNGVN	120							
Qy	121	LLQVFLSEAFWICGLRNNSGWRWDGSPLPNSRISNSSNFVOTCGAINKNGHQASCSCEVPL	180							
Db	121	LFQYVGEDFWIGLRIDIDGWRWDGSPALSLS-ILNSVYQKCGTIRHCGLHASSCEVAL	179							
Qy	181	HGVCKKV	187							
Db	180	OWICEKV	186							

```

1  RESULT 2
2  PCT-US95-04258-5
3  ; Sequence 5, Application PC/TUS9504258
4  ; GENERAL INFORMATION:
5  ; APPLICANT:
6  ; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
7  ; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (WATA)
8  ; NUMBER OF SEQUENCES: 10
9  ; CORRESPONDENCE ADDRESS:
10 ; ADDRESSEE: BROWDY AND NEIMARK
11 ; STREET: 419 Seventh Street, N.W., Suite 300
12 ; CITY: Washington
13 ; STATE: D.C.
14 ; COUNTRY: USA
15 ; ZIP: 20004
16 ; COMPUTER READABLE FORM:
17 ; MEDIUM TYPE: Floppy disk
18 ; COMPUTER: IBM PC compatible
19 ; OPERATING SYSTEM: PC-DOS/MS-DOS
20 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
21 ; CURRENT APPLICATION DATA:
22 ; APPLICATION NUMBER: PCT/US95/04258
23 ; FILING DATE: 06-APR-1995
24 ; PRIOR APPLICATION DATA:
25 ; APPLICATION NUMBER: IL 109257
26 ; FILING DATE: 08-APR-1994
27 ; ATTORNEY/AGENT INFORMATION:
28 ; NAME: BROWDY, Roger L.
29 ; REGISTRATION NUMBER: 25,618
30 ; REFERENCE/DOCKET NUMBER: PECHT=1 PCT
31 ; TELECOMMUNICATION INFORMATION:
32 ; TELEPHONE: 202-628-5197
33 ; TELEFAX: 202-737-3528
34 ; TELEX: 248633
35 ; INFORMATION FOR SEQ ID NO: 5:
36 ; SEQUENCE CHARACTERISTICS:
37 ; LENGTH: 188 amino acids
38 ; TYPE: amino acid
39 ; TOPOLOGY: linear
40 ; MOLECULE TYPE: protein
41 PCT-US95-04258-5

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Query Match      51.4%; Score 525.5; DB 5; Length 188;
Best Local Similarity 53.5%; Pred. No. 1.1e-48;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1

QY 1 MTDSVIYSMLEPTATQAONDYGPQOKSSSPSSCSCLVAITGLLTAVLLSVLLYQWLL 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MADNSIYSTLELPAAPRVQDDSRWKVKVALHHRPCVSYLVMVALGLLTIVLMSLLLYQRTL 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 61 CGGSNYSTCASCPSCDPRWKVGNHCYIYSVEKOWNSSLERCLARDSHLLVITDNOEMS 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 CCGSGKGFMCQSCRCFNLMWRNGSHCYIYSFMKRDWNSSLKFCADKXSHLLTFPPDRQGVN 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

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QY      121 LLQVFLSEAFCTGLRNNSCWWRWEDGSPLEFSRISSTSVFOTCGAINKNGLOASSCEVPL 180
       ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      121 LFOEYVGEDFYIWLGRIDIGRWWDGPALSL-ILSNSVVKCGTIHRCGLHASCEVAL 179

QY      181 HGVCCKV 187
       :|||
Db      180 QWICEKV 186
       :|||

RESULT 3
US-09-531-056A-23
; Sequence 23, Application US/09531056A
; Patent No. 6455683
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SO
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531,056A
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 23
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-531-056A-23

Query Match          42.0%; Score 430; DB 4; Length 76;
Best Local Similarity 98.7%; Pred. No. 6e-39;
Matches              75; Conservative    1; Mismatches   1; Indels     0; Gaps      0

QY      73 PSCDRMMKYNHCYTSVEEKDWNSSLEFCARDSHLLVTIDNQEMSLLOVFLSEAFCW 132
       |DCCDDRMKKNYTYSVEEYKQWNSLFFETAPDSHVAVITDNOFMSILOVFLSEAFCW 60

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1 RESULT 4
2 US-08-722-126A-6
3 ; Sequence 6, Application US/08722126A
4 ; Patent No. 6034227
5 ;
6 ; GENERAL INFORMATION:
7 ;
8 ; APPLICANT: PECHT, Israel
9 ;
10 ; APPLICANT: GUTHMANN, Marcelo D.
11 ;
12 ; APPLICANT: TAL, Michael
13 ;
14 ; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
15 ;
16 ; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
17 ;
18 ; NUMBER OF SEQUENCES: 20
19 ;
20 ; CORRESPONDENCE ADDRESS:
21 ;
22 ; ADDRESS: BROWDY AND NEIMARK, P.L.C.
23 ;
24 ; STREET: 419 Seventh Street N.W., Ste. 300
25 ;
26 ; CITY: Washington
27 ;
28 ; STATE: D.C.
29 ;
30 ; COUNTRY: UNITED STATES OF AMERICA
31 ;
32 ; ZIP: 20004
33 ;
34 ; COMPUTER READABLE FORM:
35 ;
36 ; MEDIUM TYPE: Floppy disk
37 ;
38 ; COMPUTER: IBM PC compatible
39 ;
40 ; OPERATING SYSTEM: PC-DOS/MS-DOS
41 ;
42 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
43 ;
44 ; CURRENT APPLICATION DATA:
45 ;
46 ; APPLICATION NUMBER: US/08/722,126A
47 ;
48 ; FILING DATE: 08-OCT-1996
49 ;
50 ; CLASSIFICATION: 536
51 ;
52 ; PRIOR APPLICATION DATA:
53 ;
54 ; APPLICATION NUMBER: PCT/US95/04258
55 ;
56 ; FILING DATE: 06-APR-1995
57 ;
58 ; PRIOR APPLICATION DATA:
59 ;
60 ; APPLICATION NUMBER: IL 109257

```

Query Match 36.2%; Score 370.5; DB 3; Length 114;
Best Local Similarity 58.4%; Pred. No. 2.6e-32; Indels 1; Gaps 1;
Matches 66; Conservative 18; Mismatches 28; Indels 1; Gaps 1;
QY 75 CPDRMKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMSLQVFLSEAFQWIG 134
Db 1 CPNLWNRNGSHCYFYSMEKRDWNSSLKFCADKGSLLTFPPDQGVNLFQYVVGDFYWG 60
QY 135 LRNSGWRWEDGSPINFSRISNSFVOTCGAINKGLQASSCEVPLHGVCKV 187
Db 61 LRIDIDGWRWEDGPALSLS-ILSNSVYQKGTTHRCGLHASSCEVALQWICEKV 112

RESULT 5

PCT-US95-04258-6
Sequence 6, Application PC/TUS9504258
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECHT=1 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04258-6

Query Match 36.2%; Score 370.5; DB 5; Length 114;
Best Local Similarity 58.4%; Pred. No. 2.6e-32; Indels 1; Gaps 1;
Matches 66; Conservative 18; Mismatches 28; Indels 1; Gaps 1;
QY 75 CPDRMKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMSLQVFLSEAFQWIG 134
Db 1 CPNLWNRNGSHCYFYSMEKRDWNSSLKFCADKGSLLTFPPDQGVNLFQYVVGDFYWG 60
QY 135 LRNSGWRWEDGSPINFSRISNSFVOTCGAINKGLQASSCEVPLHGVCKV 187
Db 61 LRIDIDGWRWEDGPALSLS-ILSNSVYQKGTTHRCGLHASSCEVALQWICEKV 112

RESULT 6

US-08-690-095-9
Sequence 9, Application US/08690095
Patent No. 5792648
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,095
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0110 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1098617
US-08-690-095-9

Query Match 19.2%; Score 196.5; DB 1; Length 179;
Best Local Similarity 32.7%; Pred. No. 2.4e-13;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;
QY 35 CSCIVATILGLTAVLLSVLLVQWILCOGSN--YSTCASCPCSPDRMKYGNHCYFVSVE 92
Db 20 CLSLMA-TLIGLLKNSFTKLSTPEFTPGNTELOKSDCCSQBKWGVRCNCFISSE 78
QY 93 EXDWNSSLEFCLARDSHLLVITDQEMSLQVFLSEAFQWIGL---RNSGWRWEDGSP 149
Db 79 QKTWNEHRLCASQKSSLLQLQNTDELDFMS--SSQQFYWIGLSYEETHTAWLWENGSA 136
QY 150 NFSRISSNSF---VQTCGAINKNG-LQASSCEVPLHGVCKK 186
Db 137 --SQVLFPSFETFTKNCIAYNPNGNALDESCEDEKRNRYICKQ 176

```
RESULT 7
US-08-650-578-2
; Sequence 2, Application US/08650578
; Patent No. 5811284
; GENERAL INFORMATION:
; APPLICANT: Chang, Chiwen
; APPLICANT: Aramburu Beltran, Jose
; APPLICANT: Lopez-Botet, Miguel
; APPLICANT: Phillips Jr., Joseph H.
; APPLICANT: Lanier, Lewis L.
; TITLE OF INVENTION: Purified Mammalian NK Antigens and
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650,578
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,339
; FILING DATE: 29-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin F.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-650-578-2

Query Match          19.2%; Score 196.5; DB 2; Length 179;
Best Local Similarity 32.7%; Pred. No. 2.4e-13;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCIVAITGLLTAVLLSVLLYQWILCOGNS--YSTCASCPCPDPRWKYGNHCYFSVE 92
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 20 CLSLMA-TLGILLKNSFTKLSIEPAFTPGNIELQKSDCCSCQEKWVGRCNCYFISSE 78
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 93 EKDNSSLEFCLARDSHLLVITDNQEMSLQVFLSEAFWIGL---RNNSGRWEDGSP 149
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 79 QKTWNESRHLCAQKSSLLQNTDELDFMS--SSQOFYWIGLSYSEHTAWLWENGSA 136
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 150 NFRISNSNF-----VQTCGAINKNG-LQASSCEVPLHGVCCK 186
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 137 --SQYLPSPETETNTKNCIAYNPNGNALDESCDKNRYICKQ 176
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
US-08-688-342-3
; Sequence 3, Application US/08688342
; Patent No. 5871964
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
```

```
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/688,342
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098616
US-08-688-342-3

Query Match          19.2%; Score 196.5; DB 2; Length 179;
Best Local Similarity 32.7%; Pred. No. 2.4e-13;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCIVAITGLLTAVLLSVLLYQWILCOGNS--YSTCASCPCPDPRWKYGNHCYFSVE 92
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 20 CLSLMA-TLGILLKNSFTKLSIEPAFTPGNIELQKSDCCSCQEKWVGRCNCYFISSE 78
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 93 EKDNSSLEFCLARDSHLLVITDNQEMSLQVFLSEAFWIGL---RNNSGRWEDGSP 149
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 79 QKTWNESRHLCAQKSSLLQNTDELDFMS--SSQOFYWIGLSYSEHTAWLWENGSA 136
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 150 NFRISNSNF-----VQTCGAINKNG-LQASSCEVPLHGVCCK 186
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 137 --SQYLPSPETETNTKNCIAYNPNGNALDESCDKNRYICKQ 176
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9
US-09-113-788-3
; Sequence 3, Application US/09113788
; Patent No. 5969104
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
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/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/113,788
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/688,342
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 179 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 1098616
/ US-09-113-788-3

Query Match 19.2%; Score 196.5; DB 2; Length 179;
Best Local Similarity 32.7%; Pred. No. 2.4e-13;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCLVAITLGLTAVLLSVLLYQWILCOGSN--YSTCASCPCSPDRMVKYGNHCYFVSVE 92
Db 20 CLSLMA-TLIGLLKNSFTKLSIEPATPGNIELQKSDCCSQCKWVGRCNCYFISSE 78

QY 93 EKDNSSLEFCLARDSHLIVITDNOEMSLLOVFLSEAFWIGL---RNNSGRWEDGSP 149
Db 79 QKTWNEHRLCASQKSLLOLQNTDLDLDFMS--SSQCFYWIGLSYEHTAWLWENGSA 136

QY 150 NFRSISSNF---VOTCGAINKNG-LQASSCEVPLHGVCCK 186
Db 137 --SQYLPSPFETNTKNCIAYNPNGNALDESCEDKNRYICKQ 176

RESULT 10
US-09-113-789-9
/ Sequence 9, Application US/09113789
/ Patent No. 6034219
/ GENERAL INFORMATION:
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Au-Young, Janice
/ APPLICANT: Goli, Surya K.
/ TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: U.S.
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/113,789
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/690,095

/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/113,788
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/688,342
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 179 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 1098616
/ US-09-113-788-3

Query Match 19.2%; Score 196.5; DB 3; Length 179;
Best Local Similarity 32.7%; Pred. No. 2.4e-13;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCLVAITLGLTAVLLSVLLYQWILCOGSN--YSTCASCPCSPDRMVKYGNHCYFVSVE 92
Db 20 CLSLMA-TLIGLLKNSFTKLSIEPATPGNIELQKSDCCSQCKWVGRCNCYFISSE 78

QY 93 EKDNSSLEFCLARDSHLIVITDNOEMSLLOVFLSEAFWIGL---RNNSGRWEDGSP 149
Db 79 QKTWNEHRLCASQKSLLOLQNTDLDLDFMS--SSQCFYWIGLSYEHTAWLWENGSA 136

QY 150 NFRSISSNF---VOTCGAINKNG-LQASSCEVPLHGVCCK 186
Db 137 --SQYLPSPFETNTKNCIAYNPNGNALDESCEDKNRYICKQ 176

RESULT 11
US-08-772-440-17
/ Sequence 17, Application US/08772440
/ Patent No. 6046158
/ GENERAL INFORMATION:
/ APPLICANT: Ariizumi, Kiyoshi
/ APPLICANT: Takashima, Akira
/ TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
/ TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
/ TITLE OF INVENTION: THEREOF
/ NUMBER OF SEQUENCES: 42
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: USA
/ ZIP: 77210
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/772,440
/ FILING DATE: CONCURRENTLY HERewith
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Parker, David L.
/ REGISTRATION NUMBER: 32,165
/ REFERENCE/DOCKET NUMBER: UTXD:493
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512/418-3000
/ TELEFAX: 512/474-7577
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
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; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-772-440-17

Query Match
Best Local Similarity 17.2%; Score 175.5; DB 3; Length 168;
Matches 42; Conservative 28; Mismatches 51; Indels 27; Gaps 4;

QY 25 QOKSSSKPSCSLVAITLGLTAVLLS-----VLLYQWILCOGS-----NYSTCA 70
Db 3 QERQSGKGVCTWLRWLSAAVISMLLSTCTFIASCVTYQFIMQPSRRLYELHTYHSSL 62
QY 71 SCPS-----CPDRWKYGNHCYFVSVEKDWNSLSEFLCLARDSHLLVITDNOE 118
Db 63 TCFSEGTVMSEKMGCCNHNKWSFGSSCYLLSTKENFWSTSEQNCVQMGHLLVINTAE 122
QY 119 MSLIQVFLSEAFW-IGLRNNSGWRWED 145
Db 123 QNFITQQLNESLSYFLGLSNPKNKGWND 150

RESULT 12
US-08-772-440-15
; Sequence 15, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Ariizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DEXTIN-1 AND DEXTIN-2; COMPOSITIONS AND USES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-772-440-15

Query Match
Best Local Similarity 16.9%; Score 173; DB 3; Length 175;
Matches 52; Conservative 34; Mismatches 64; Indels 38; Gaps 9;

QY 25 QOKSSSKPSCSLVAITLGLTAVLLSVLLYQWILCOGSNYSTC--ASCPS-----CPD 77
Db 3 QERQSGKGVCTWLRWLSAAVISMLLSTCTFIASCVTYQFIMQPSRRLYELHTYHSSL 47

US-08-772-440-16
; Sequence 16, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Ariizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DEXTIN-1 AND DEXTIN-2; COMPOSITIONS AND USES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-772-440-16

Query Match
Best Local Similarity 16.8%; Score 172; DB 3; Length 134;
Matches 42; Conservative 26; Mismatches 43; Indels 26; Gaps 6;

QY 25 QOKSSSKPSCSLVAITLGLTAVLLSVLLYQWILCOGSNYSTC--ASCPS-----CPD 77
Db 3 QERQSGKGVCTWLRWLSAAVISMLLSTCTFIASCVTYQFIMQPSRRLYELHTYHSSL 47
QY 78 RMKYGNHCYFVSVEKDWNSLSEFLCLARDSHLLVITDNOEMLLQVFLSEAFW-IGL- 135
Db 48 HWSFGSSCYLLSTKENFWSTSEQNCVQMGHLLVINTAEQNFITQQLNESLSYFLGLS 107
QY 136 --RNNSGWRWEDGSPN-----FSRISNSFVQTGAI-----NKGILQASCEVPLHGV 183
Db 108 DPQNGKQWIDDTFFSQNVRFWHPHPNLPPEERCVSIVYWNPSKMGWNDVFCDSKHNSI 167
QY 184 C--KKVRL 189
Db 168 CEMKKIYL 175

RESULT 13
US-08-772-440-16
; Sequence 16, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Ariizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DEXTIN-1 AND DEXTIN-2; COMPOSITIONS AND USES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-772-440-16

Query Match
Best Local Similarity 16.8%; Score 172; DB 3; Length 134;
Matches 42; Conservative 26; Mismatches 43; Indels 26; Gaps 6;

QY 25 QOKSSSKPSCSLVAITLGLTAVLLSVLLYQWILCOGSNYSTC--ASCPS-----CPD 77
Db 3 QERQSGKGVCTWLRWLSAAVISMLLSTCTFIASCVTYQFIMQPSRRLYELHTYHSSL 47
QY 78 RMKYGNHCYFVSVEKDWNSLSEFLCLARDSHLLVITDNOEMLLQVFLSEAFW-IGL- 135
Db 48 HWSFGSSCYLLSTKENFWSTSEQNCVQMGHLLVINTAEQNFITQQLNESLSYFLGLS 107
QY 136 --RNNSGWRWEDGSPN-----FSRISNSFVQTGAI-----NKGILQASCEVPLHGV 183
Db 108 DPQNGKQWIDDTFFSQNVRFWHPHPNLPPEERCVSIVYWNPSKMGWNDVFCDSKHNSI 167
QY 184 C--KKVRL 189
Db 168 CEMKKIYL 175

RESULT 14
```

US-08-543-246B-18
; Sequence 18, Application US/08543246B
; Patent No. 6262244
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA and amino acid sequence specific for
; natural killer cells
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michael W. Glynn
; STREET: 564 Morris Avenue
; CITY: Summit,
; STATE: NJ
; COUNTRY: US
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/543,246B
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,663
; FILING DATE: 28-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02469
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,514
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kassenoff, Melvyn M.
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-522-6927
; TELEFAX: 908-522-6955
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
; US-08-543-246B-18
; Query Match 16.6%; Score 169.5; DB 3; Length 120;
; Best Local Similarity 31.6%; Pred. No. 1.1e-10;
; Matches 37; Conservative 20; Mismatches 55; Indels 5; Gaps 3;
QY 72 CPSPDRWKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQMSLLQVFLSEAF 131
Db 3 CGHCPEWITYNSCYIGKERTWEESLLACTSKNSLLSIDNEEMKFLSIIPSS-- 60
QY 132 WIGL-RNNSGWRWEDGSPLNFSR--ISSNSFVQTGAINKNGLOASSCEVPLHGVC 185
Db 61 WIGVFRNSSHHPTWMTNGLAFLKHEIKDSNAELNCAVLQVNRKLSAQCGSSIIYHCK 117
RESULT 15
US-08-543-246B-17
; Sequence 17, Application US/08543246B
; Patent No. 6262244
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA and amino acid sequence specific for
; natural killer cells

; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michael W. Glynn
; STREET: 564 Morris Avenue
; CITY: Summit,
; STATE: NJ
; COUNTRY: US
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/543,246B
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,663
; FILING DATE: 28-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02469
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,514
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kassenoff, Melvyn M.
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-522-6927
; TELEFAX: 908-522-6955
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
; US-08-543-246B-17
; Query Match 16.6%; Score 169.5; DB 3; Length 135;
; Best Local Similarity 31.6%; Pred. No. 1.3e-10;
; Matches 37; Conservative 20; Mismatches 55; Indels 5; Gaps 3;
QY 72 CPSPDRWKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQMSLLQVFLSEAF 131
Db 18 CGHCPEWITYNSCYIGKERTWEESLLACTSKNSLLSIDNEEMKFLSIIPSS-- 75
QY 132 WIGL-RNNSGWRWEDGSPLNFSR--ISSNSFVQTGAINKNGLOASSCEVPLHGVC 185
Db 76 WIGVFRNSSHHPTWMTNGLAFLKHEIKDSNAELNCAVLQVNRKLSAQCGSSIIYHCK 132
Search completed: August 10, 2004, 16:35:49
Job time : 18 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:39:40 ; Search time 13.5 Seconds

(without alignments)
1339.556 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029

Sequence: 1 MADSSYSTLELPEAPQVOD.....GLQASSCEVALQWICKKVLV 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 95185

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: Pirl:*

2: pirl2:*

3: pirl3:*

4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	838	81.4	188	2 I59421	mast cell function
2	163.5	15.9	146	2 JC7135	agkisacutacin beta
3	155.5	15.1	156	2 T28141	C type lectin, B1
4	152.5	14.8	146	2 JC4691	coagulation factor
5	146.5	14.2	146	2 JC7105	aggreitin beta chai
6	138	13.4	167	1 WMVZF2	hepatic lectin hom
7	136.5	13.3	170	2 T28140	natural killer cel
8	135	13.1	144	2 PC7027	aggreitin alpha cha
9	119	11.6	133	2 A47267	botrocetin alpha c
10	117.5	11.4	123	2 B42972	coagulation factor
11	114.5	11.1	152	2 JC7134	agkisacutacin alph
12	113.5	11.0	125	2 B47267	botrocetin beta ch
13	109.5	10.6	155	2 S78774	perilucin - Haloti
14	107.5	10.4	116	1 WMVZF8	hepatic lectin hom
15	105.5	10.3	125	2 JC5059	bitiscetin beta ch
16	104	10.1	152	2 JC4690	coagulation factor
17	103	10.0	175	2 S29822	pancreatitits-assoc
18	102.5	10.0	162	1 LNR3	lectin BRAJ-2 prec
19	101.5	9.9	123	2 JC2415	echicetin beta cha
20	101.5	9.9	162	1 LNR3	lectin BRAJ-1 prec
21	101	9.8	175	2 A49616	pancreatitits-assoc
22	97.5	9.5	165	2 A28351	pancreatit stone p
23	97	9.4	135	2 A38609	lectin, galactose-
24	95	9.2	174	2 S54979	pancreatitits-assoc
25	94	9.1	175	2 A41719	pancreatit stone p
26	93	9.0	163	1 A43413	antifreeze protein
27	91	8.8	129	2 JC4329	coagulation factor
28	90.5	8.8	166	2 A45751	pancreatit stone p
29	90	8.7	131	2 JC5058	bitiscetin alpha c

30 90 8.7 166 1 RGHU1A regenerating islet
31 89.5 8.7 166 1 RGHU1B regenerating islet
32 86 8.4 174 2 I83377 regenerating prote
33 86 8.4 175 2 A37194 pancreatic thread
34 85 8.3 40 2 S56007 tokaracatin beta c
35 81.5 7.9 143 1 WMVZEL hepatic lectin hom
36 81 7.9 165 2 A47148 reg I, regeneratin
37 80.5 7.8 142 2 S78596 ovocleidin - chick
38 79 7.7 40 2 B56829 alboaggregin-B alp
39 79 7.7 140 2 JC7786 lectin CEL-I, N-ac
40 78 7.6 174 1 A48689 pancreatitis-assoc
41 77.5 7.5 173 2 S10548 lectin - barnacle
42 76 7.4 159 2 T30745 hypothetical prote
43 75.5 7.3 147 2 A26697 echinoidin - sea u
44 75 7.3 166 2 T28809 hypothetical prote
45 75 7.3 173 2 B47148 reg II, regenerati

ALIGNMENTS

RESULT 1

I59421
mast cell function associated antigen - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I59421
R:Guthmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A:Title: A secretion inhibitory signal transduction molecule on mast cells is another C.
A:Reference number: I59421; MUID:96016176; PMID:7568140
A:Accession: I59421
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-188 <RES>
A:Cross-references: EMBL:X79812; NID:gi:020141; PIDN:CAA56208.1; PID:gi020142
C:Genetics:
A:Gene: mafa

Query Match 81.4%; Score 838; DB 2; Length 188;
Best Local Similarity 80.7%; Pred. No. 1.3e-74;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADSSYSTLELPEAPQVODSRWKLKAVLHHPHLSRFAMVALGLLTIVLSLLMYQRTIL 60
DB 1 MADSSYSTLELPEAPRVQDDSRWKKVAVLHHPHLSRFAMVALGLLTIVLSLLMYQRTIL 60
QY 61 CCGSKDSTCSHCPCPILWTRNGSHCYFYSMEKKDWNSSLKFCADKSGHLLTPPDNQGVK 120
DB 61 CCGSKGFMCSCSRCPENLWNRNGSHCYFYSMEKKDWNSSLKFCADKSGHLLTPPDNQGVN 120
QY 121 LFEYGLQDFYWGILNRIDGWEGGPAALSILNTLSLQRCGAHNRGLQASSCEVALQ 180
DB 121 LFEQYVGDFYWGILNRIDGWEDGPAALSILNSVYVQCGTTHRCGLHASSCEVALQ 180
QY 181 WICKKVL 187
DB 181 WICEKVL 187

RESULT 2

JC7135
agkisacutacin beta chain precursor - sharp-nosed viper
N:Alternate names: fibrinogenlytic venom protein
C:Species: Agkistrodon acutus (sharp-nosed viper)
C:Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000
C:Accession: JC7135; PC7038
R:Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
Biochem. Biophys. Res. Commun. 265, 530-535, 1999
A:Title: Purification, characterization, and cDNA cloning of a new fibrinogenlytic venom
A:Reference number: JC7134; MUID:20025379; PMID:10558903
A:Accession: JC7135
A:Molecule type: mRNA

A;Residues: 1-146 <CHE>
A;Cross-references: GB:AF176421
A;Experimental source: venom gland
A;Accession: PC7038
A;Molecule type: protein
A;Residues: 24-50:59-83;102-107;112-114 <CH2>
C;Superfamily: tetranectin; C-type lectin homolog
C;Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-146/Product: agkiscutacin beta chain #status experimental <MAT>

Query Match 15.9%; Score 163.5; DB 2; Length 146;
Best Local Similarity 30.2%; Pred. No. 1e-08;
Matches 48; Conservative 15; Mismatches 71; Indels 25; Gaps 6;

QY 35 LSRFAMVALGLTIVLMSLLMYQRLCCGSKDSTCSHCPCPILWTRNGSHCYFYSMEKK 94
Db 1 MGRFIFVSGLLVVFV-----SLSGTAADCP-----EWSSYEGHCYKPFDEPK 44

QY 95 DWNSSLKFCAD--KGSHLLTFPDNQG---VKLFGEYLGQDFYWIGLRNI-DG--WRWEG 145
Db 45 TWADAERFCTQKHGSHLAFHSSEADFFVTLTPSLKTLVWIGLNWNGCYWKSND 104

QY 146 GPALSRLITNSLQRCGALHNRGLQASCEVALQWICK 184
Db 105 GTKLDYKDWRECFECLVSRVTNNEWLSMDCGTTCSPVCK 143

RESULT 3
T28141
C type lectin, B locus - chicken
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T28141
R;Milne, S.; Kaufman, J.; Beck, S.
submitted to the EMBL Data Library, May 1998
A;Description: DNA sequencing and analysis of the chicken major histocompatibility complex
A;Reference number: Z20475
A;Accession: T28141
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-156 <ML>
A;Cross-references: EMBL:AL023516; NID:el292539; PID:el292545; PIDN:CAAL8961.1
A;Experimental source: clone c812
C;Genetics:
A;Gene: Blec
A;Map position: 16
A;Introns: 17/1; 74/3; 110/2

Query Match 15.1%; Score 155.5; DB 2; Length 156;
Best Local Similarity 25.0%; Pred. No. 6.7e-08;
Matches 39; Conservative 24; Mismatches 68; Indels 25; Gaps 6;

QY 39 AMVALGLTIVLMSLLMYQRLCCGSKDSTCSH---CPCPILWTRNGSHCYFYSMEKKD 95
Db 3 AVFTVLITAVAFVAQFQ-----PHQPQCAQCFDWMIGPRGKCYFSEDSN 50

QY 96 WNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNIDG---WRWEGPALS- 150
Db 51 WTSQNNCSALGASLAFDSAEIDLFTMRHKGSSPHWGLSR-EGKEHPWENRSPLSH 109

QY 151 -LRILNLSLQRCGALHNRGLQASCEVALQWICK 185
Db 110 LFQVQGDGL---CAYLGDAGLSHSGSTRNRNVCTK 142

RESULT 4
JC4691
coagulation factor IX/factor X-binding protein chain A precursor - habu
C;Species: Trimeresurus flavoviridis (habu)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Jun-2000
C;Accession: JC4691; B39332; JC4330
R;Matsuzaki, R.; Yoshihara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.

Biochem. Biophys. Res. Commun. 220, 382-387, 1996
A;Title: cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from
A;Reference number: JC4690; MUID:96184662; PMID:8645314
A;Accession: JC4691
A;Molecule type: mRNA
A;Residues: 1-146 <MAT1>
A;Cross-references: DDBJ:D83332; NID:g1402641; PIDN:BAA11888.1; PID:g1402642
A;Experimental source: venom
R;Atoda, H.; Hyuga, M.; Morita, T.
J. Biol. Chem. 266, 14903-14911, 1991
A;Title: The primary structure of coagulation factor IX/factor X-binding protein isolated
A;Title: tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E.
A;Reference number: A39332; MUID:91332000; PMID:1831197
A;Accession: B39332
A;Molecule type: protein
A;Residues: 24-146 <AT0>
R;Atoda, H.; Ishikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T.
J. Biochem. 118, 965-973, 1995
A;Title: Blood coagulation factor IX-binding protein from the venom of Trimeresurus flavoviridis
A;Reference number: JC4329; MUID:96318509; PMID:8749314
A;Accession: JC4330
A;Molecule type: protein
A;Residues: 24-146 <AT2>
C;Superfamily: tetranectin; C-type lectin homolog
C;Keywords: anticoagulant; blood coagulation; lectin; venom
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-146/Product: factor IX/X binding protein chain B #status predicted <MAT>
F;25-142/Domain: C-type lectin homolog <ICH>
F;25-36,53-142,119-134/Disulfide bonds: #status predicted

Query Match 14.8%; Score 152.5; DB 2; Length 146;
Best Local Similarity 24.5%; Pred. No. 1.2e-07;
Matches 39; Conservative 25; Mismatches 70; Indels 25; Gaps 5;

QY 35 LSRFAMVALGLTIVLMSLLMYQRLCCGSKDSTCSHCPCPILWTRNGSHCYFYSMEKK 94
Db 1 MGRFIFVSGLLVVFV-----SLSGTAADCPD---WSSYEGHCYKPFSEPK 44

QY 95 DWNSSLKFCADK--GSHLLTFPDNQG---VKLFGEYLGQDFYWIGLRNI---DGWREG 145
Db 45 NWADAENFCTQKHAGHLSVFSQSEADFFVVKLAFQTFGHSIFWMLGSLNVMQCNWQSN 104

QY 146 GPALSRLITNSLQRCGALHNRGLQASCEVALQWICK 184
Db 105 AMLRYKAWAESYCYFYSKSTNNKRSRACRMAQFVCE 143

RESULT 5
JC7105
aggrexin beta chain - Malayan pit viper
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C;Accession: JC7105
R;Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A;Title: Molecular cloning and sequence analysis of aggrexin, a collagen-like platelet
A;Reference number: PC7027; MUID:99443731; PMID:10512747
A;Accession: JC7105
A;Molecule type: mRNA
A;Residues: 1-146 <CHU>
A;Experimental source: venom gland
C;Superfamily: tetranectin; C-type lectin homolog
C;Keywords: disulfide bond; platelet aggregation; venom

Query Match 14.2%; Score 146.5; DB 2; Length 146;
Best Local Similarity 29.0%; Pred. No. 4.7e-07;
Matches 47; Conservative 18; Mismatches 66; Indels 31; Gaps 8;

QY 35 LSRFAMVALGLTIVLMSLLMYQRLCCGSKDSTCSHCPCPILWTRNGSHCYFYSMEKK 94
Db 1 MGRFIFVSGLLVVFV-----SLSGTADCFSG---WSSYEGHCYKPFSEPK 44

QY 95 DWNSSLKFC--ADKSHLLTFPDNQG---VKLFGEYLGQDFYWIGLRNI---DGWREG 145

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Db      107 WIGLEVSTNQMKVDNDSYNSTEDNLSVMEN-----RCGFFKNTKVEGDVCSGEHQMVCQ 163
QY      185 K 185
Db      163 K 163

RESULT 8
PC7027
aggreitin alpha chain - Malayan pit viper (fragment)
C:Species: Calloselasma rhodostoma (Malayan pit viper)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C:Accession: PC7027
R:Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A:Title: Molecular cloning and sequence analysis of aggreitin, a collagen-like
A:Reference number: PC7027; MUID:99443731; PMID:10512747
A:Accession: PC7027
A:Molecule type: mRNA
A:Residues: 1-144 <CHU>
A:Experimental source: venom gland
C:Superfamily: tetranectin; C-type lectin homology
C:Keywords: disulfide bond; platelet aggregation; venom

Query Match      13.1%; Score 135; DB 2; Length 144;
Best Local Similarity 25.5%; Pred. No. 6.3e-06;
Matches 36; Conservative 23; Mismatches 64; Indels 18; Gaps 5

QY      66 DSTCHCHSPCLITWRNTHSGHYYSMEKKDWNLSKFC--ADKGSLLITFDNQGVKLF 123
Db      4 EGTRAGLEDCDFGSPFYDQHCYQAFNEQKTDWEAEKFCRAQENGHAHLASIESNGEADFVS 63
QY      124 -----EYIGDFFWIGLRNID-----GWEGEGPALSRLILNSLIQRCGAHR-NGL 170
Db      64 WLISQKDELADEYVWIGLRQNKEQQCSSEWSGSSVSYENLIDLTKKGALEKLTGF 123
QY      171 QA-----SSCEVALQWICKKVLV 188
Db      124 RKWNVNYCBQMEAFVCKLPY 144

RESULT 9
A47267
botrocetin alpha chain - jararaca
N:Alternate names: two chain botrocetin alpha chain
C:Species: Bothrops jararaca (jararaca)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998
C:Accession: A47267; B37958
R:Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993
A:Title: Primary structure of two-chain botrocetin, a von Willebrand factor mo
A:Reference number: A47267; MUID:93157385; PMID:8430107
A:Accession: A47267
A:Molecule type: protein
A:Molecule type: protein
A:Residues: 1-133 <USA>
A:Experimental source: venom
A:Note: sequence extracted from NCBI backbone (NCBIP:124085)
R:Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui
Biochemistry 30, 1957-1964, 1991
A:Title: Isolation and chemical characterization of two structurally and funct
A:Reference number: A37958; MUID:91129280; PMID:1993206
A:Accession: B37958
A:Molecule type: protein
A:Residues: 1-40 <FOU>
C:Complex: heterodimer of alpha and beta (see PIR:B47267) chains
C:Superfamily: tetranectin; C-type lectin homology
C:Keywords: hemaagglutinin; heterodimer; venom
F:2-128/Domain: C-type lectin homology <LCH>
F:2-133,30-128,103-120/Disulfide bonds: #status experimental
F:80/Disulfide bonds: interchain (to beta-75) #status experimental

Query Match      11.6%; Score 119; DB 2; Length 133

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Best Local Similarity 25.4%; Pred. No. 0.00021;
Matches 29; Conservative 26; Mismatches 33; Indels 26; Gaps 7;
QY 75 CPILWTRNGSHCYFMSMEKKDWSLSKFCAD--KGSHLLTFPDNGVKLFG---EYLG-- 127
DB 2 CPDWSVSEGCYKFFQGMWADAEFCSEQAKGHLVS-----IKIYSKEKDFVGD 55
QY 128 -----QDFY-WIGLR--NID--GMPWEGGPALSLRLTNSLIQRCGAH 168
DB 56 VTKNIQSSDLXAWIGLRVNEKEKQCSSESDGSSVSVENVETVKKCFAL 109
RESULT 10
B42972
coagulation factor X activating enzyme (EC 3.4.24.-) light chain - Russell's viper
C;Species: Vipera russelli (Russell's viper)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997
C;Accession: B42972
R;Takeya, H.; Nishida, S.; Miyata, T.; Kawada, S.; Saisaka, Y.; Morita, T.; Iwanaga, S.
J. Biol. Chem. 267, 14109-14117, 1992
A;Title: Coagulation factor X activating enzyme from Russell's viper venom (RVV-X). A no
A;Reference number: A42972; MUID:92332516; PMID:1629211
A;Contents: V. x. siamensis
A;Accession: B42972
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-123 <TAK>
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:108408)
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: hydrolase; metalloproteinase; venom; zinc
F;4-121/Domain: C-type lectin homology <LCH>
F;4-15,32-121,98-113/Disulfide bonds: #status predicted
Query Match 11.4%; Score 117.5; DB 2; Length 123;
Best Local Similarity 26.4%; Pred. No. 0.00027;
Matches 32; Conservative 15; Mismatches 61; Indels 13; Gaps 4;
QY 75 CPILWTRNGSHCYFMSMEKKDWSLSKFCAD--KGSHLLTFPDNGQ---VKLFGVYLQ 128
DB 4 CPDWSVSEGCYKFFQGMWADAEFCSEQAKGHLVS-----IKIYSKEKDFVGD 53
QY 129 DFVWIGLRNIDGWR-----MEGGPALSRLTNSLIQRCGAHNGIQASCEVALOWIC 183
DB 64 PATWIGLGNM--WKDCRMENSDRGVVKYKALAEESYCLIMITHEKEWKMTCNFIAPVVC 121
QY 184 K 184
DB 122 K 122
RESULT 11
JC7134
agkisacutacin alpha chain precursor - sharp-nosed viper
N;Alternate names: fibrinogenolytic venom protein
C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000
C;Accession: JC7134; PC7037
R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
Biochem. Biophys. Res. Commun. 265, 530-535, 1999
A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenolytic venom
A;Reference number: JC7134; MUID:20025379; PMID:10558903
A;Accession: JC7134
A;Molecule type: mRNA
A;Residues: 1-152 <CHE>
A;Cross-references: GB:AF176420
A;Experimental source: venom gland
A;Accession: PC7037
A;Molecule type: protein
A;Residues: 24-53;84-86;87-94;125-136;137-152 <CH2>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-152/Product: agkisacutacin alpha chain #status experimental <MAT>
Query Match 11.1%; Score 114.5; DB 2; Length 152;
Best Local Similarity 23.6%; Pred. No. 0.00067;
Matches 35; Conservative 18; Mismatches 60; Indels 35; Gaps 6;
QY 35 LSRFAMVALGLTLVILMSLLMYQRIICGSKDSCSCPCPILWTRNGSHCYFMSMEKK 94
DB 1 MGRFIFVSFGLLVVFL-----SLSGTAADCSG---WSSVEGHCYKVFVKQSK 44
QY 95 DWSNLSKFCADK--GSHLLTFPDNGVKLFGVYLQDP-----YWIGLR-----NI 138
DB 45 TWADAESFCTKQVNGGHLVSISSGEADFAVHLIAQKISAKIHVWIGLRQAKKEKQCSI 104
QY 139 DGWMEGGPALSRLTNSLIQRCGAH 166
DB 105 E---WSDGSSISVENWIEESKKCLGVH 129
RESULT 12
B47267
botrocetin beta chain - jararaca
N;Alternate names: two chain botrocetin beta chain
C;Species: Bothrops jararaca (Jararaca)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998
C;Accession: B47267; C37958
R;Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993
A;Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator p
A;Reference number: A47267; MUID:93157385; PMID:8430107
A;Accession: B47267
A;Molecule type: protein
A;Residues: 1-125 <USA>
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:124086)
R;Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Su
Biochemistry 30, 1957-1964, 1991
A;Title: Isolation and chemical characterization of two structurally and functionally
A;Reference number: A37958; MUID:91129280; PMID:1993206
A;Accession: C37958
A;Molecule type: protein
A;Residues: 1-40 <FU>
C;Complex: heterodimer of alpha (see PIR:A47267) and beta chains
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: hemagglutinin; heterodimer; venom
F;2-121/Domain: C-type lectin homology <LCH>
F;2-13,30-121,98-113/Disulfide bonds: #status experimental
F;75/Disulfide bonds: interchain (to alpha-80) #status experimental
Query Match 11.0%; Score 113.5; DB 2; Length 125;
Best Local Similarity 31.3%; Pred. No. 0.00069;
Matches 26; Conservative 12; Mismatches 32; Indels 13; Gaps 4;
QY 75 CPILWTRNGSHCYFMSMEKKDWSLSKFCADK--GSHLLTFPDNGQV----KLFGEVYLQ 128
DB 2 CPDWSVSEGCYKFFQGMWADAEFCSEQAKGHLVS-----IKIYSKEKDFVGD 61
QY 129 DFVWIGLRNIDGWR-----RWEGG 146
DB 62 DVVWIGLSDV--WNKCRFEWTDG 82
RESULT 13
S78774
Perlucin - Haliotis laevigata
C;Species: Haliotis laevigata
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 17-Mar-2000
C;Accession: S78774
R;Mann, K.
submitted to the Protein Sequence Database, January 2000
A;Reference number: S78774
A;Contents: S78774
A;Accession: S78774